

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 10, 2005, 11:21:18 ; Search time 3299 Seconds
(without alignments)
1662.808 Million cell updates/sec

Title: US-10-659-782A-32

Perfect score: 616

Sequence: 1 MSPSGTVCSSLLGLMLWLDL.....PFSSRRSRSSHQSCSPSL 116

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-O=/cn2 1/USPTO spoal/US10659782/runat_05022005 161917 4270/app query.fasta_1.263
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOEFL=0 -LOEPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10659782 @CN 1 1 3731 @runat 05022005 161917 4270 -NCPU=6 -ICPU=3
-NO MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DSV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:*
1: gb.ba:*
2: gb.htg:*
3: gb.in:*
4: gb.om:*
5: gb.ov:*
6: gb.pat:*
7: gb.ph:*
8: gb.pl:*
9: gb.pr:*
10: gb.ro:*
11: gb.sts:*
12: gb.sy:*
13: gb.un:*
14: gb.vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	605.5	98.3	507	11	G72347 ghrelin xl-
2	605.5	98.3	5199	9	AF296558 Homo sapi
3	605.5	98.3	104947	9	AC008116 Homo sapi
4	605.5	98.3	146947	2	AC012515 Homo sapi

c	5	605.5	98.3	210053	9	AC022384	AC022384 Homo sapi
c	6	605.5	98.3	216292	2	AC012600	AC012600 Homo sapi
c	7	605.5	98.3	217778	9	AC090841	AC090841 Homo sapi
	8	500.5	81.2	6008	9	AY372274	AY372274 Macaca mu
	9	220.5	35.8	362	4	AY455990	AY455990 Caracus el
	10	214.5	34.8	354	4	AY455987	AY455987 Odocoileu
	11	214	34.7	351	6	AR170496	AR170496 Sequence
	12	214	34.7	351	6	AR208181	AR208181 Sequence
	13	214	34.7	351	6	AR404108	AR404108 Sequence
	14	214	34.7	351	6	AX062356	AX062356 Sequence
	15	214	34.7	351	6	AX154581	AX154581 Sequence
	16	214	34.7	351	6	BD061161	BD061161 Motilin h
	17	214	34.7	402	9	AY184207	AY184207 Homo sapi
	18	214	34.7	511	6	CQ722673	CQ722673 Sequence
	19	214	34.7	511	6	CQ794618	CQ794618 Sequence
	20	214	34.7	511	6	BD012137	BD012137 Novel pep
	21	214	34.7	511	9	AB029434	AB029434 Homo sapi
	22	214	34.7	519	9	HS4252278	HS4252278 Homo sapi
	23	214	34.7	526	6	BD222667	BD222667 Human sig
	24	214	34.7	527	6	AX356127	AX356127 Sequence
	25	214	34.7	542	9	BC025791	BC025791 Homo sapi
	26	214	34.7	654	6	AR252557	AR252557 Sequence
	27	214	34.7	654	6	AX403380	AX403380 Sequence
	28	214	34.7	654	6	AX464308	AX464308 Sequence
	29	214	34.7	654	9	AY359053	AY359053 Homo sapi
	30	212.5	34.5	362	4	AY455994S1	AY455994 Odocoileu
	31	209.5	34.0	362	4	AY455988S1	AY455988 Rangifer
	32	208.5	33.8	479	9	AB035700	AB035700 Homo sapi
	33	208.5	33.8	508	6	BD012139	BD012139 Novel pep
	34	207	33.6	354	9	AY371699	AY371699 Macaca mu
	35	205	33.3	410	4	AY422043S1	AY422043 Sus scrof
	36	203	33.0	233811	10	AC117596	AC117596 Mus muscu
	37	197.5	32.1	4513	10	AB060078	AB060078 Mus muscu
	38	194	31.5	643	4	AB089201	AB089201 Felis cat
	39	192.5	31.2	362	4	AY455985S1	AY455985 Capra hir
	40	192.5	31.2	640	4	AB089202	AB089202 Felis cat
	41	190	30.8	366	4	AY455979S1	AY455979 Bos tauru
	42	190	30.8	366	4	AY455981S1	AY455981 Kogia bre
	43	180	29.2	324	4	AY455992S1	AY455992 Alces alc
	44	178	28.9	366	4	AY454076S1	AY454076 Bison bis
	45	178	28.9	487	6	CQ794617	CQ794617 Sequence

ALIGNMENTS

RESULT 1
G72347
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

G72347
ghrelin X1-2 Human Homo sapiens STS genomic, sequence tagged site.
G72347
G72347.1 GI:14518296
STS.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Cox,D.G., Boillot,C. and Canzian,F.
Genome Survey
Unpublished (2000)

Contact: Federico Canzian
Genome Analysis Group
International Agency for Research on Cancer
150, cours Albert-Thomas, F-69372 Lyon Cedex 08 France
Tel: +33-4-72738698
Fax: +33-4-72738388
Email: canzian@iarc.fr
Primer A: AGACCTCTCTCTCCCCAG
Primer B: TCCTCGCTGCCACAGAG
STS size: 507
Protocol:
Template: 50 ng

Primer: 4 uM each
 dNTPs: 2 mM each
 MgCl2: 1.5-2.5 mM
 Tag: 0.05 units
 Total Vol: 25 uL

Buffer: 1.5-2.5 mM
 MgCl2: 50 mM
 KCl: 20 mM
 Tris-HCl: 8.4.
 pH:

FEATURES
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 /mol_type="genomic DNA"
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 1..507
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 primer_bind complement(490..507)
 ORIGIN

Alignment Scores:
 Pred. No.: 9,896-43 Length: 507
 Score: 605.50 Matches: 116
 Percent Similarity: 99.15% Conservative: 0
 Best Local Similarity: 99.15% Mismatches: 0
 Query Match: 98.30% Indels: 1
 DB: 11 Gaps: 1

US-10-659-782A-32 (1-116) x G72347 (1-507)

QY 1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTripleuAspLeu 20
 Db 48 ATGCCCTCCCGAGGACGCTGCGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 107
 QY 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
 Db 108 GCATGGAGGAGGCTTCCAGCTTCTGAGCCTTGACACCGAGAGTCCAGGTGAGACTCTCC 167
 QY 41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
 Db 168 CACAAGCCCAACATGTTGTTCCAGCCCTGCCACTTAGCAACCACTCTGTGACCTGGAG 227
 QY 61 GlnGlnArgHis---TrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAsp 79
 Db 228 CAGCAGCGCATCTCTGGGCTTTCAGTCTTCTCCAGAGCACAAAGGACTCTGGGTCTGAC 287
 QY 80 LeuThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProSer 99
 Db 288 CTCACCTGTTCTGGAGGACATGGGGGCTTAGAGTCTTAAACAGACTGTTTCCCTCTCC 347
 QY 100 SerArgGluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
 Db 348 AGCAGAGAAAGGAGTCCGAGAGAGCCAGCAGCCAGCTGAGCCCGAGGCTC 398

RESULT 2
 AF296558
 LOCUS
 DEFINITION Homo sapiens growth hormone secretagogue precursor (GHRELIN) gene,
 complete cds.
 ACCESSION AF296558
 VERSION AF296558.1 GI:9966512
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 5199)
 Wajnrach,M.P., Ten,I.S., Gertner,J.M. and Leibel,R.L.
 TITLE Genomic Organization of the human GHRELIN gene
 JOURNAL J. Endocr. Genet. 1, 231-233 (2000)
 REFERENCE 2 (bases 1 to 5199)

AUTHORS Wajnrach,M.P., Ten,I.S., Gertner,J.M. and Leibel,R.L.
 TITLE Direct Submission
 JOURNAL Submitted (15-AUG-2000) Pediatrics, Weill Medical College of
 Cornell University, 525 East 68th Street, Room M-624, New York, NY
 10021, USA

FEATURES
 Location/Qualifiers
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 /chromosome="3"
 /map="3p26-p25"
 /clone="BAC CTB-187Pl"
 1..5199
 /gene="GHRELIN"
 /note="GHS"
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 1..554
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 /protein_id="AAG10300.1"
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 /translation="MPSPTVCSSLLLMLMLDLAMAGSSFLSPHQVQORKESSKPK
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 /number=1
 749..865
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 /number=2
 752..865
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 866..3813
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 3814..3922
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 4752..5199
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ORIGIN
 Alignment Scores:
 Pred. No.: 1,02e-41 Length: 5199
 Score: 605.50 Matches: 116
 Percent Similarity: 99.15% Conservative: 0
 Best Local Similarity: 99.15% Mismatches: 0
 Query Match: 98.30% Indels: 1
 DB: 9 Gaps: 1

US-10-659-782A-32 (1-116) x AF296558 (1-5199)

QY 1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
 Db 447 ATGCCCTCCCGAGGACCGCTCTGAGCTCTCTCTGCGCATGCTCTGGCTGGACTTG 506
 QY 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
 Db 507 GCCATGGCAGGCTCCAGCTTCTGAGCCCTGAAACACGAGAGTCCAGGTGAGACTCCC 566
 QY 41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
 Db 567 CACAAAGCCCCCATGTTTCCAGCCCTGCCACTTAGCACACGACTCTGTGACCTGGAG 626
 QY 61 GlnGlnArgHis---TrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAsp 79
 Db 627 CAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCAGAGCAGACAAAGGACTCTGGTCTGAC 686
 QY 80 LeuThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSer 99
 Db 687 CTCACCTGTTTCTGGAAGGACATGGGGCTTAGAGTCTCTAAACAGACTGTTTCCCTCTCC 746
 QY 100 SerArgGluArgSerArgGlyHisGlnProSerCysSerProGluLeu 116
 Db 747 AGCAGAAAGGAGTCAAGAGCCACACGACCCAGCTGAGCCCGAGCTC 797

RESULT 3

AC008116/c

LOCUS AC008116 104947 bp DNA linear PRI 15-MAR-2002
 DEFINITION Homo sapiens 3p25-26 BAC CTB-187P1 (California Institute of Technology BAC Library) complete sequence.
 ACCESSION AC008116
 VERSION AC008116.8 GI:6001959
 KEYWORDS HTG.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 104947)
 AUTHORS Muzny, D.M., Adams, C., Bailey, M., Barber, J., Blankenburg, K., Bork, B., Bouck, J., Bowie, S., Brooks, A., Buhay, C., Bunac, C., Burdett, C., Burrows, J., Carter, M., Chacko, J., Chen, Z., Cox, C., David, R., Delgado, O., Deshazo, D., Ding, Y., Domagala-Rashid, N., Dugan-Rocha, S., Durbin, K.J., Fernandez, C., Ferraguto, D., Forcum-Tansey, J., Frantz, P., Ganes, R., Garcia, D.K., Gorrell, J.H., Gorrell, L.L., Guevara, W., Harris, K., He, X., Hernandez, J., Hodgson, A., Hughes, M., Holloway, C., Hosak, H., Jackson, L.E., Jackson, L., Jia, Y., Jones, M., Kelly, S., Kondrjewski, N., Kong, Y., Kovar, C., Leal, B., Li, Z., Lichtarge, O., Liu, J., Liu, W., Logan, O., Lu, J., Lucier, R., Martin, R., Martinez, C., McLeod, M.P., Mei, G., Moore, S., Moorish, T., Morgan, M., Morris, S., Nash, S., Nelson, A., Nguyen, R., Nguyen, N., Nguyen, S., Osval, G., Parish, B., Paxton, S., Payton, B., Perez, L., Pu, L.L., Quiles, M., Reller, D., Rives, M., Samuel, S., Say, J., Scherer, S., Shah, E., Shen, H., Simon, M., Sparks, A., Stamps, A., Sugang, R., Tabor, P., Taylor, T., Vasquez, L., Vinson, R., Vo, Q., Wabnah, M., Watlington, S., Weinstein, G., Weinstein, I.R., Williamson, A., Worley, K., Wren, J., Wrensford, G., Yu, W., Zhou, X., Naylor, S.L., Nelson, D. and Gibbs, R.

TITLE JOURNAL

REFERENCE 2 (bases 1 to 104947)

Worley, K.C.

Direct Submission

TITLE JOURNAL
 Submitted (24-JUL-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 REFERENCE 3 (bases 1 to 104947)

Worley, K.C.

Direct Submission

TITLE JOURNAL
 Submitted (30-SEP-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 REFERENCE 4 (bases 1 to 104947)

AUTHORS

TITLE JOURNAL

REFERENCE 5 (bases 1 to 104947)

Worley, K.C.

Direct Submission

TITLE JOURNAL

Submitted (11-JUL-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 REFERENCE 6 (bases 1 to 104947)

Worley, K.C.

Direct Submission

TITLE JOURNAL

Submitted (15-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 On Sep 30, 1999 this sequence version replaced gi:5882338.
 INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least 2 exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

QUALSTAT-REPORT-----

Summary Statistics

Contig length: 104947
 Phrap values in estimate: 104295
 Average error rate (BCM-Phrap estimate): 0.000147946
 Fraction of Phrap values less than 40 : 0.0217748
 Number of consensus changing edits: 21
 Number of N's in consensus : 0

Consensus changing edits

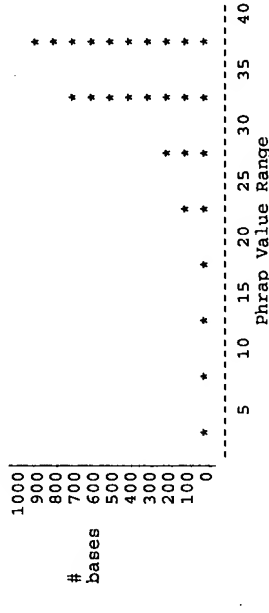
Position Original+Context Edited+Context
 13808 cctgtgtttt(n)ttttattga cctgtgtttt(t)ttttattga
 14561 gcgagctgag(t)ttacacctg gcgagctgag(g)ttacacctg
 14579 ctgcactcca(n)cctgggcaac ctgcactcca(a)cctgggcaac
 14610 ttgctctcaa(n)aaaaaatat ttgctctcaa(g)aaaaaatat

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14613 gcctcaaaaa(n)aanntatata
14616 tcaaaaaaaa(n)ttatatatat
14617 caaaaaaaa(n)ttatatatat
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15207 ttttttttt(n)ggagatggag
15242 tggagtgcag(n)ggagatctac
22275 ggcgtgagcc(n)cgccgctgg
22312 aacgtttatg(n)tgattttttt
22632 gccgggccc(n)acttttaaaa
23169 tggggaaagg(n)cgagccatct
38915 accgcctcg(n)ctcccaaaag
39053 tgggtgctca(n)ttctgtaacc
39054 ggtggctcan(n)ttctgtaacc
39079 actttggag(n)ccagggcgna
39088 gncacgggcn(n)acagatccat
77261 gagggggaga(n)agagaaagg
78454 cccgacgggc(n)gtggcgtagg

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----- Distribution of Quality < 40 Bases -----



Version: 1.01 xfgo.

FEATURES

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/chromosomes="3"
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/complement(360..561)
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643..1074
AA876147"

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repeat_region

repeat_region

misc_feature

/note="Region: Unigene cluster containing AI246590 and

repeat_region

repeat_region

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repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

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Alignment Scores:

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Pred. No.: 2.07e-40 Length: 104947
Score: 605.50 Matches: 116
Percent Similarity: 99.15% Conservative: 0
Best Local Similarity: 99.15% Mismatches: 0
Query Match: 99.30% Indels: 1
DB: 9 Gaps: 1

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US-10-659-782A-32 (1-116) x AC008116 (1-104947)

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Qy 1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
Db 47501 ATGCCCTCCCGAGGACGCTCGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 47442
Qy 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgPro 40
Db 47441 GCCATGGCAGGCTCGAGCTCTCTGAGCCCTGAAACACAGAGAGTCCAGTGGACCTCC 47382
Qy 41 HisLysAlaProHisValValProAlaLeuProLeuSerAanGlnLeuCysAspLeuGlu 60
Db 47381 CACAAGGCCACATGTTTCCAGCCCTGACCTAGCAACACAGCTCTGTGACCTGGAG 47322
Qy 61 GlnGlnArgHis-----TrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAsp 79
Db 47321 CAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCAGAGACACAAAGGACTCTGGGTCTGAC 47262
Qy 80 LeuThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProSer 99
Db 47261 CTCACTGTTTCTGAGGACATGGGGCTTAGAGTCTTAAACAGACTGTTTCCCTCTCC 47202
Qy 100 SerArgGluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
Db 47201 AGCAGAGAAAGGAGTTCGAAGAAGCCACAGCAAGCTGCAGCCCGAGCTC 47151

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RESULT 4

AC012515

LOCUS

DEFINITION

AC012515

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

REFERENCES

AUTHORS

REFERENCES

AUTHORS

REFERENCES

AUTHORS

REFERENCES

AUTHORS

REFERENCES

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AUTHORS

REFERENCES

Hollins, B., Homs, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L. E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratoch, J., Kureshi, A., Landry, N., Leal, B., Lewis, L. C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louissegh, H., Lozano, R. J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M. P., Meador, M., Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenwo, S., Ogun, M., Okunolu, G., Orangunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, D., Pickens, R., Primus, E., Pu, L. L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, R., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D., and Gibbs, R.

Direct Submission
Unpublished
2 (bases 1 to 146947)
Worley, K. C.

Direct Submission
Submitted (29-OCT-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jan 7, 2001 this sequence version replaced gi:9929498.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: HMLC
Center clone name: RP11-885J5
----- Summary Statistics
Sequencing vector: M13; L08821
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 117566 bases at least Q40
Consensus quality: 133456 bases at least Q30
Consensus quality: 137976 bases at least Q20
Estimated insert size: 138502; sum-of-contigs estimation
Estimated insert size: 207623; agarose-fp estimation
Quality coverage: 2.4x in Q20 bases; agarose-fp estimation
Quality coverage: 3.6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 16 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 42943: contig of 42943 bp in length
* 42944 43043: gap of unknown length
* 43044 65409: contig of 22366 bp in length
* 65410 65509: gap of unknown length
* 65510 82660: contig of 17151 bp in length
* 82661 82760: gap of unknown length
* 82761 96493: contig of 13733 bp in length
* 96494 96593: gap of unknown length
* 96594 105307: contig of 8714 bp in length
* 105308 105407: gap of unknown length
* 105408 111891: contig of 6474 bp in length

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

* 111882 111981: gap of unknown length
* 111982 120039: contig of 8058 bp in length
* 120039 120139: gap of unknown length
* 120140 124819: contig of 4680 bp in length
* 124820 124919: gap of unknown length
* 124920 130083: contig of 5164 bp in length
* 130084 130183: gap of unknown length
* 130184 134897: contig of 4714 bp in length
* 134898 134997: gap of unknown length
* 134998 138724: contig of 3727 bp in length
* 138725 138824: gap of unknown length
* 138825 141665: contig of 2841 bp in length
* 141666 141765: gap of unknown length
* 141766 143446: contig of 1681 bp in length
* 143447 143546: gap of unknown length
* 143547 144555: contig of 1009 bp in length
* 144556 144555: gap of unknown length
* 144556 145815: contig of 1160 bp in length
* 145816 145915: gap of unknown length
* 145916 146947: contig of 1032 bp in length.

FEATURES
Location/Qualifiers
source

1..146947
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="3"
/clone="RP11-885J5"

ORIGIN

Alignment Scores:

Pred. No.: 2,9e-40 Length: 146947
Score: 605.50 Matches: 116
Percent Similarity: 99.15% Conservative: 0
Best Local Similarity: 99.15% Mismatches: 0
Query Match: 98.30% Indels: 1
DB: 2 Gaps: 1

US-10-659-782A-32 (1-116) x AC012515 (1-146947)

Qy 1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
Db 35989 ATGCCTCCCGAGGACCGCTCTGCAGCCTCTCTCGGCATGCTCTGGCTGGACTTG 36048
Qy 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
Db 36049 GCATGGCAGGCTCCAGCTTCTTGAGCCTTGACACCAGAGAGTCCAGGTGAGACTCCC 36108
Qy 41 HisLysAlaProHisValValProLalaLeuProLalaLeuSerAsnGlnLeuCysAspLeuGlu 60
Db 36109 CACAAAGCCCAACATGTTTCCAGCCTCCACTTAGCAACAGCTCTGTGACCTGGAG 36168
Qy 61 GlnGlnArgHis---TtpAlaSerValPheSerGlnSerThrLysAspSerGlySerAsp 79
Db 36169 CAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCAGAGCACAAAGAGACTCTGGTCTGAC 36228
Qy 80 LeuThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProSer 99
Db 36229 CTCACGTGTTTCGGAAGGACATGGGGCTTAGAGTCTTAACAGACTGTTTCCCCCTTCC 36288
Qy 100 SerArgGluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
Db 36289 AGCAGAGAAAGGAGTCAAGAGAGCCAGCCAGCCAGCTGCAGCCCGGAGCTC 36339

RESULT 5
AC022384/c
LOCUS AC022384
DEFINITION Homo sapiens chromosome 3 clone RP11-438J1 map 3p, complete sequence.
ACCESSION AC022384
VERSION AC022384.5 GI:24418051
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 210053)
Chen,L., Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J.,
Ding,H., Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q., Gu,X., Guo,D.,
Guo,Z., He,L., Hu,S., Huang,F., Jin,Y., Kang,N., Li,C., Li,C.,
Li,F., Li,G., Li,L., Li,L., Li,S., Li,T., Liu,Y., Liu,N., Liu,B.,
Liu,Y., Li,W., Li,Y., Luo,J., Luo,J., Niu,Y., Qi,Q., Qi,X., Song,L.,
Song,S., Sun,M., Sun,W., Sun,Y., Tan,X., Tao,R., Wang,H., Wang,J.,
Wang,J., Wang,J., Wang,L., Wang,L., Wang,R., Wang,X., Wang,X.,
Wang,Y., Wu,D., Wu,Q., Xie,F., Xuan,Z., Xue,Y., Yan,C., Yang,X.,
Yu,B., Zeng,Y., Zhang,G., Zhang,H., Zhang,H., Zhang,L., Zhang,M.,
Zhang,X., Zhang,X., Zhang,Y., Zhang,Y., Zhang,Z., Zhu,B., Zhu,N.,
Yu,J. and Yang,H.

TITLE

JOURNAL

REFERENCE

AUTHORS

Chromosome 3p genomic sequence

2 (bases 1 to 210053)

Hu,S., Dong,W., Zhang,X., Wang,J., Zhang,Y., Zhang,H., Liu,B.,
Bao,W., Sun,Y., Wu,Q., Wang,H., Wang,X., Cheng,C., Wang,Y., Niu,Y.,
Qi,X., Li,T., Zhang,H., Liu,N., Wu,D., Yu,B., Fan,H., Liu,Y.,
Li,G., Li,C., Bao,Q., Bao,J., Wang,X., Song,L., Zhang,L., Guo,D.,
Huang,F., Zhang,G., Li,J., Bian,X., Zhang,M., Li,L., Feng,X., Yu,J.
and Yang,H.

Direct Submission
Submitted (03-FEB-2000) Human Genomic Center, Institute of
Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
100101, P.R.China

3 (bases 1 to 210053)
Chen,L., Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J.,
Ding,H., Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q., Gu,X., Guo,D.,
Guo,Z., He,L., Hu,S., Huang,F., Jin,Y., Kang,N., Li,C., Li,C.,
Li,F., Li,G., Li,J., Li,L., Li,L., Li,S., Li,T., Liu,Y., Liu,N., Liu,B.,
Liu,Y., Li,W., Li,Y., Luo,J., Luo,J., Niu,Y., Qi,Q., Qi,X.,
Song,L., Song,S., Sun,M., Sun,W., Sun,Y., Tan,X., Tao,R., Wang,H.,
Wang,J., Wang,J., Wang,L., Wang,L., Wang,R., Wang,X., Wang,X.,
Wang,Y., Wu,D., Wu,Q., Xie,F., Xuan,Z., Xue,Y., Yan,C.,
Yang,X., Yu,B., Zeng,Y., Zhang,G., Zhang,H., Zhang,L., Zhang,M.,
Zhang,X., Zhang,X., Zhang,Y., Zhang,Y., Zhang,Z., Zhu,B.,
Zhu,N., Yu,J. and Yang,H.

Direct Submission
Submitted (16-JAN-2001) Human Genomic Center, Institute of
Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
100101, P.R.China

4 (bases 1 to 210053)
Chen,L., Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J.,
Ding,H., Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q., Gu,X., Guo,D.,
Guo,Z., He,L., Hu,S., Huang,F., Jin,Y., Kang,N., Li,C., Li,C.,
Li,F., Li,G., Li,L., Li,L., Li,S., Li,T., Liu,Y., Liu,N., Liu,B.,
Liu,Y., Li,W., Li,Y., Luo,J., Luo,J., Niu,Y., Qi,Q., Qi,X., Song,L.,
Song,S., Sun,M., Sun,W., Sun,Y., Tan,X., Tao,R., Wang,H., Wang,J.,
Wang,J., Wang,L., Wang,L., Wang,R., Wang,X., Wang,X., Wang,Y.,
Wu,D., Wu,Q., Xie,F., Xuan,Z., Xue,Y., Yan,C., Yang,X., Yu,B.,
Zeng,Y., Zhang,G., Zhang,H., Zhang,H., Zhang,L., Zhang,M.,
Zhang,X., Zhang,X., Zhang,Y., Zhang,Y., Zhang,Z., Zhu,B., Zhu,N.,
Yu,J. and Yang,H.

Direct Submission
Submitted (29-OCT-2002) Human Genomic Center, Institute of
Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
100101, P.R.China

5 (bases 1 to 210053)
Chen,L., Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J.,
Ding,H., Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q., Gu,X., Guo,D.,
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Li,F., Li,G., Li,L., Li,L., Li,S., Li,T., Liu,Y., Liu,N., Liu,B.,
Liu,Y., Li,W., Li,Y., Luo,J., Luo,J., Niu,Y., Qi,Q., Qi,X., Song,L.,
Song,S., Sun,M., Sun,W., Sun,Y., Tan,X., Tao,R., Wang,H., Wang,J.,
Wang,J., Wang,L., Wang,L., Wang,R., Wang,X., Wang,X., Wang,Y.,
Wu,D., Wu,Q., Xie,F., Xuan,Z., Xue,Y., Yan,C., Yang,X., Yu,B.,
Zeng,Y., Zhang,G., Zhang,H., Zhang,H., Zhang,L., Zhang,M.,
Zhang,X., Zhang,X., Zhang,Y., Zhang,Y., Zhang,Z., Zhu,B., Zhu,N.,
Yu,J. and Yang,H.

Direct Submission
Submitted (08-NOV-2002) Human Genomic Center, Institute of

Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
100101, P.R.China
On Oct 29, 2002 this sequence version replaced gi:12232490.

COMMENT

Center: Beijing Center
Website: http://hgsc.igtp.ac.cn
http://www.genomics.org.cn
Contact: hgsc@igtp.ac.cn
----- Project Information
Center project name: 116 project
Center clone name: RP11-438J1
----- Summary Statistics
Sequencing vector: pUC18; 100% of reads
Chemistry: Dye-terminator; ET 55% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 212148 bases at least Q40
Consensus quality: 213483 bases at least Q30
Consensus quality: 214138 bases at least Q20
Insert size: 210053; sum-of-contigs
Quality coverage: 11.98x in Q20 bases; sum-of-contigs

FEATURES

source

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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="3"
/map="3p"
/clone="RP11-438J1"

ORIGIN

Alignment Scores:

Pred. No.: 4.14e-40 Length: 210053
Score: 605.50 Matches: 116
Percent Similarity: 99.15% Conservative: 0
Best Local Similarity: 99.15% Mismatches: 0
Query Match: 98.30% Indels: 1
DB: Gaps: 1

US-10-659-782A-32 (1-116) x AC022384 (1-210053)

QY

1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTriLeuAspLeu 20
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QY

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169322 GCCATGGCAGGCTCCAGCTTCTGTAGCCCTGAACACACAGAGAGTCCAGGTGAGACTCCC 169263

QY

41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
169262 CACAAGAGCCACATGTTGTTCCAGCCTGACCTAGCAACACAGCTCTGTGACCTGGAG 169203

QY

61 GlnGlnArgHis---TtpAlaSerValPheSerGlnSerThrLysAspSerGlySerAsp 79
169202 CAGCAGCCCATCTCTGGGCTTCAGTCTTCCACAGACACAAAGACTCTGGGCTGAC 169143

QY

80 LeuThrValSerGlyValThrTrpGlyLeuArgValLeuAsnArgLeuPheProSer 99
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QY

100 SerArgGluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
169082 AGCAGAGAAAGAGTTCGAAGAAGCCAGCCAGCTCAGCCCGAGCTC 169032

RESULT 6

AC012600/c

LOCUS

DEFINITION

SEQUENCE, 11 unordered pieces.

AC012600

AC012600

216292 bp DNA linear HTG 04-SEP-2000
Homo sapiens chromosome 3 clone RP1-1082A18, WORKING DRAFT
AC012600

VERSION
KEYWORDS
SOURCE
ORGANISM

AC012600.10 GI:9966203
HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 216292)

REFERENCE
AUTHORS

Muzny, D.M., Adams, C., Bailey, M., Barbara, J., Blankenburg, K.,
Bodota, B., Bouck, J., Bowie, S., Brooks, A., Buhay, C., Bunac, C.,
Burkett, C., Burrows, J., Carter, M., Chacko, J., Chen, J., Cox, C.,
David, R., Delgado, O., Deshazo, D., Ding, Y., Domah-Rashid, N.,
Dugan-Rocha, S., Durbin, K.J., Fernandez, C., Ferraguto, D.,
Forcum-Tansey, J., Frantz, P., Ganesh, R., Gorrell, J.H., Gorrell, L.L.,
Guevara, W., Harris, K., Hernandez, J., Hodgson, A., Hognes, M.,
Holloway, C., Hosak, H., Jackson, L.E., Jackson, L., Jia, Y., Jones, M.,
Kelly, S., Kondejewski, N., Kong, Y., Kovar, C., Leal, B., Li, Z.,
Lichtarge, O., Liu, J., Liu, W., Logan, O., Lozano, R.J., Lu, J.,
Lucier, R., Martin, R., Martinez, C., McLeod, M.P., Mei, G., Morgan, M.,
Morris, S., Nash, S., Nelson, A., Nguyen, R., Nguyen, N., Nguyen, S.,
Oswal, G., Parish, B., Paxton, S., Payton, B., Perez, L., Pu, L.L.,
Quiles, M., Reiter, D., Rives, M., Samuel, S., Say, J., Scherex, S.,
Shah, E., Shen, H., Simon, M., Sparks, A., Stamps, A., Sugeng, R.,
Tabor, P., Taylor, T., Vasquez, L., Vinson, R., Vo, O., Wabba, M.,
Watlington, S., Weinstein, G., Weinstein, I.R., Williamson, A., and
Worley, K., Wren, J., Wrensford, G., Yu, W., Zhou, X., Nelson, D., and
Gibbs, R.

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

Direct Submission
Unpublished
2 (bases 1 to 216292)
Worley, K.C.
Direct Submission
Submitted (31-OCT-1999) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Sep 4, 2000 this sequence version replaced gi:9719583.
----- Genome Center

Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: HMGN
Center clone name: RP1-1082A18
----- Summary Statistics

Sequencing vector: M13; L08821
Chemistry: Dye-terminator Big Dye; 98% of reads
Assembly program: Phrap; version 0.90329
Consensus quality: 193458 bases at least Q40
Consensus quality: 207037 bases at least Q30
Consensus quality: 210993 bases at least Q20
Estimated insert size: 213807; sum-of-contigs estimation
Estimated insert size: 317914; agarose-fp estimation
Quality coverage: 3x in Q20 bases; agarose-fp estimation
Quality coverage: 4.4x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 11 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 84660: contig of 84660 bp in length
* 84661 84760: gap of unknown length
* 141893 141893: contig of 57133 bp in length
* 141894 141993: gap of unknown length
* 141994 157877: contig of 15884 bp in length
* 157878 157977: gap of unknown length
* 157978 173668: contig of 15791 bp in length
* 173669 173868: gap of unknown length

* 173869 185178: contig of 11310 bp in length
* 185179 185278: gap of unknown length
* 185279 192013: contig of 6735 bp in length
* 192014 192113: gap of unknown length
* 192114 196844: contig of 4731 bp in length
* 196845 196944: gap of unknown length
* 196945 205362: contig of 8418 bp in length
* 205363 205463: gap of unknown length
* 205463 210832: contig of 5370 bp in length
* 210833 210933: gap of unknown length
* 210933 214884: contig of 3952 bp in length
* 214885 214985: gap of unknown length
* 214986 216292: contig of 1308 bp in length.

FEATURES
Source

Location/Qualifiers
1..216292
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="3"
/clone="RP1-1082A18"

ORIGIN

Alignment Scores:
Pred. No.: 4,278-40 Length: 216292
Score: 605.50 Matches: 116
Percent Similarity: 99.15% Conservative: 0
Best Local Similarity: 99.15% Mismatches: 0
Query Match: 98.30% Indels: 1
DB: 2 Gaps: 1

US-10-659-782A-32 (1-116) x AC012600 (1-216292)

QY 1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
Db 164737 ATGCGCTCCCGAGGACCGCTGCGAGCTCTCTCGGATGCTCTGGTGGACTTG 164678
QY 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
Db 164677 GCATGGCAGGCTCCAGCTTCTGAGCCTTGAACACAGAGAGTCCAGGTGAGACTCC 164618
QY 41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
Db 164617 CACAAGGCCCCACATGTGTTCCAGCCTGCCACCTAGCAACAGACTCTGTGACCTGGAG 164558
QY 61 GlnGlnArgHis---TrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAsp 79
Db 164557 CAGCAGGCCCATCTCTGGGCTTCAGTCTTCTCCAGAGCACAAGGACTCTGGGCTGAC 164498
QY 80 LeuThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProSer 99
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QY 100 SerArgGluArgSerArgSerHisGlnProSerCysSerProGluLeu 116
Db 164437 AGCAGAAAGAGGAGTGAAGAGCCAGCCAGCTGAGCCCGGAGCTC 164387

RESULT 7

AC090841/c
LOCUS AC090841 217778 bp DNA linear PRI 08-NOV-2002
DEFINITION Homo sapiens chromosome 3 clone RP11-1082A18 map 3p, complete
sequence.
ACCESSION AC090841
VERSION AC090841.2 GI:24418046
KEYWORDS HTG
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 217778)
Zhang, L., Bao, J., Bao, Q., Bao, W., Bian, X., Cao, T., Chen, C.,
Chen, J., Ding, H., Dong, W., Fan, H., Feng, X., Gong, J., Guan, Q.,
Gu, X., Guo, D., Guo, Z., He, D., Hu, S., Huang, F., Jin, Y., Kang, N.,
Li, C., Li, C., Li, F., Li, G., Li, J., Li, L., Li, S., Li, T., Liu, Y.,

Liu, N., Liu, B., Liu, Y., Li, W., Li, W., Li, Y., Luo, J., Niu, Y., Qi, Q., Qi, X., Song, L., Song, S., Sun, M., Sun, W., Sun, Y., Tan, X., Tao, R., Wang, H., Wang, J., Wang, J., Wang, J., Wang, L., Wang, L., Wang, R., Wang, X., Wang, X., Wang, Y., Wu, D., Wu, Q., Xie, F., Xuan, Z., Xue, Y., Yan, C., Yang, X., Yu, B., Zeng, X., Zhang, G., Zhang, H., Zhang, H., Zhang, M., Zhang, X., Zhang, X., Zhang, Y., Zhang, Y., Zhang, Z., Zhu, B., Zhu, N., Yu, J. and Yang, H.

Chromosome 3p genomic sequence

Unpublished

2 (bases 1 to 217778)

Zhang, L., Bao, J., Bao, Q., Bao, W., Bian, X., Cao, T., Chen, C., Chen, J., Ding, H., Dong, W., Fan, H., Feng, X., Gong, J., Guan, Q., Gu, X., Guo, D., Guo, Z., He, L., Hu, S., Huang, F., Jin, Y., Kang, N., Li, C., Li, C., Li, F., Li, G., Li, J., Li, L., Li, S., Li, T., Liu, Y., Liu, N., Liu, B., Liu, Y., Li, W., Li, W., Li, Y., Luo, C., Luo, J., Niu, Y., Qi, Q., Qi, X., Song, L., Song, L., Song, S., Sun, M., Sun, W., Sun, Y., Tan, X., Tao, R., Wang, H., Wang, J., Wang, J., Wang, L., Wang, L., Wang, R., Wang, X., Wang, X., Wang, Y., Wu, D., Wu, Q., Xie, F., Xuan, Z., Xue, Y., Yan, C., Yang, X., Yu, B., Zeng, X., Zhang, G., Zhang, H., Zhang, H., Zhang, M., Zhang, X., Zhang, X., Zhang, Y., Zhang, Y., Zhang, Z., Zhu, B., Zhu, N., Yu, J. and Yang, H.

Direct Submission

Submitted (11-MAR-2001) Human Genomic Center, Institute of Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing 100101, P.R.China

3 (bases 1 to 217778)

Zhang, L., Bao, J., Bao, Q., Bao, W., Bian, X., Cao, T., Chen, C., Chen, J., Ding, H., Dong, W., Fan, H., Feng, X., Gong, J., Guan, Q., Gu, X., Guo, D., Guo, Z., He, L., Hu, S., Huang, F., Jin, Y., Kang, N., Li, C., Li, C., Li, F., Li, G., Li, J., Li, L., Li, S., Li, T., Liu, Y., Liu, N., Liu, B., Liu, Y., Li, W., Li, W., Li, Y., Luo, J., Niu, Y., Qi, Q., Qi, X., Song, L., Song, S., Sun, M., Sun, W., Sun, Y., Tan, X., Tao, R., Wang, H., Wang, J., Wang, J., Wang, L., Wang, L., Wang, R., Wang, X., Wang, X., Wang, Y., Wu, D., Wu, Q., Xie, F., Xuan, Z., Xue, Y., Yan, C., Yang, X., Yu, B., Zeng, X., Zhang, G., Zhang, H., Zhang, H., Zhang, M., Zhang, X., Zhang, X., Zhang, Y., Zhang, Y., Zhang, Z., Zhu, B., Zhu, N., Yu, J. and Yang, H.

Direct Submission

Submitted (29-OCT-2002) Human Genomic Center, Institute of Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing 100101, P.R.China

4 (bases 1 to 217778)

Zhang, L., Bao, J., Bao, Q., Bao, W., Bian, X., Cao, T., Chen, C., Chen, J., Ding, H., Dong, W., Fan, H., Feng, X., Gong, J., Guan, Q., Gu, X., Guo, D., Guo, Z., He, L., Hu, S., Huang, F., Jin, Y., Kang, N., Li, C., Li, C., Li, F., Li, G., Li, J., Li, L., Li, S., Li, T., Liu, Y., Liu, N., Liu, B., Liu, Y., Li, W., Li, W., Li, Y., Luo, J., Niu, Y., Qi, Q., Qi, X., Song, L., Song, S., Sun, M., Sun, W., Sun, Y., Tan, X., Tao, R., Wang, H., Wang, J., Wang, J., Wang, L., Wang, L., Wang, R., Wang, X., Wang, X., Wang, Y., Wu, D., Wu, Q., Xie, F., Xuan, Z., Xue, Y., Yan, C., Yang, X., Yu, B., Zeng, X., Zhang, G., Zhang, H., Zhang, H., Zhang, M., Zhang, X., Zhang, X., Zhang, Y., Zhang, Y., Zhang, Z., Zhu, B., Zhu, N., Yu, J. and Yang, H.

Direct Submission

Submitted (08-NOV-2002) Human Genomic Center, Institute of Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing 100101, P.R.China

On Oct 29, 2002 this sequence version replaced gi:13273353.

-----Genome Center

Center: Beijing Center

Center code: Beijing

Website: <http://hgci.igtp.ac.cn>

<http://www.genomics.org.cn>

Contact: hgc@igtp.ac.cn

-----Project Information

Center project name: 1% project

Center clone name: RP11-1082A18

----- Summary Statistics

Sequencing vector: pUC18; 100% of reads

Chemistry: Dye-terminator; BT 55% of reads

Chemistry: Dye-terminator; Big Dye; 45% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 956 bases at least Q40

Consensus quality: 1239 bases at least Q30
Consensus quality: 1436 bases at least Q20
Insert size: 1445; sum-of-contigs
Quality coverage: 1.32x in Q20 bases, sum-of-contigs

FEATURES

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Query Match: 98.30% Indels: 1
Gaps: 1

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QY 61 GlnGlnArgHis---TtpAlaSerValPheSerGlnSerThrLysAspSerGlySerAsp 79
Db 7995 CAGCAGCCCATCTCTGGGCTTCACTTCTCCAGACACACAGAGCTCTGGGTCTGAC 7936
QY 80 LeuThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProSer 99
Db 7935 CTCACCTGTTCTGGAAGGACATGGGGCTTAGAGTCTTAAACAGACTGTTCCCGCTTCC 7876
QY 100 SerArgGluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
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RESULT 8

AY372274

LOCUS Macaca mulatta ghrelin precursor (GHRL) gene, complete cds.
DEFINITION Macaca mulatta ghrelin precursor (GHRL) gene, complete cds.
ACCESSION AY372274
VERSION AY372274.1 GI:34541889

KEYWORDS

SOURCE

ORGANISM

Macaca mulatta (rhesus monkey)

Macaca mulatta

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

Cercopithecinae; Macaca.

1 (bases 1 to 6008)

Angeloni, S.V., Glynn, N., Ambrosini, G., Garant, M.J., Dee Higley, J.,

Suomi, S. and Hansen, B.C.

Characterization of the rhesus monkey ghrelin gene and factors

influencing ghrelin gene expression and fasting plasma levels

Endocrinology 145 (5), 2197-2205 (2004)

14736731

2 (bases 1 to 6008)

Angeloni, S.V., Glynn, N.M., Ambrosini, G., Garant, M.J., Higley, J.D.,

Suomi, S. and Hansen, B.C.

Direct Submission

Submitted (21-AUG-2003) Center for Vaccine Development, University

1

Percent Similarity: 44.44% Conservative: 1
 Best Local Similarity: 43.59% Mismatches: 0
 Query Match: 34.74% Indels: 65
 DB: 6 Gaps: 1

US-10-659-782A-32 (1-116) x AR208181 (1-351)

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QY 41 HisLysAlaProHisValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
 Db 108 ----- 108

QY 61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
 Db 108 ----- 108

QY 81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100
 Db 108 ----- 108

QY 101 Arg-GluArgSerArgSerHisGlnProSerCysSerProGluLeu 116
 Db 109 CAGAGAAGAGTCCGAGAAGCCACCCAGCTCAAGCTGCGAGCTC 157

RESULT 13
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 LOCUS
 DEFINITION Sequence 1 from patent US 6627729.
 ACCESSION AR404108.1 GI:40152102
 VERSION AR404108.1
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 351)
 AUTHORS Sheppard,P.O., Deisher,T.A., Jaspers,S.R. and Bishop,P.D.
 TITLE TML peptides
 JOURNAL Patent: US 6627729-A 1 30-SEP-2003;
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 Score: 214.00 Matches: 51
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QY 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
 Db 61 GCCATGGCAGGCTCCAGCTCTCTGAGCCCTGAACACAGAGAGTCCAG----- 108

QY 41 HisLysAlaProHisValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
 Db 108 ----- 108

QY 61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
 Db 108 ----- 108

QY 81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100
 Db 108 ----- 108

QY 101 Arg-GluArgSerArgSerHisGlnProSerCysSerProGluLeu 116
 Db 109 CAGAGAAGAGTCCGAGAAGCCACCCAGCTCAAGCTGCGAGCTC 157

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 ACCESSION AX062356
 VERSION AX062356.1 GI:12540240
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Sheppard,P.O., Jaspers,S.R., Deisher,T.A. and Bishop,P.D.
 TITLE Sgip peptides
 JOURNAL Patent: WO 0100830-A 3 04-JAN-2001;
 ZymoGenetics, Inc. (US)
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ORIGIN
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 Pred. No.: 1.18e-09 Length: 351
 Score: 214.00 Matches: 51
 Percent Similarity: 44.44% Conservative: 1
 Best Local Similarity: 43.59% Mismatches: 0
 Query Match: 34.74% Indels: 65
 DB: 6 Gaps: 1

US-10-659-782A-32 (1-116) x AX062356 (1-351)

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QY 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
 Db 61 GCCATGGCAGGCTCCAGCTCTCTGAGCCCTGAACACAGAGAGTCCAG----- 108

QY 41 HisLysAlaProHisValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
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QY 61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
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Search completed: February 10, 2005, 15:18:58
Job time : 3413 secs

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RESULT 15
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LOCUS AX154581 351 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1 from Patent WO0138355.
ACCESSION AX154581
VERSION AX154581.1 GI:14536167
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 Sheppard, P.O., Jaspers, S.R., Deisher, T.A. and Bishop, P.D.
  TITLE Method of forming a peptide-receptor complex with zsig33 and
  JOURNAL therapeutic use thereof
  Patent: WO 0138355-A 1 31-MAY-2001;
  ZymoGenetics, Inc. (US)
FEATURES
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ORIGIN
Alignment Scores:
Pred. No.: 1.18e-09 Length: 351
Score: 214.00 Matches: 51
Percent Similarity: 44.44% Conservative: 1
Best Local Similarity: 43.59% Mismatches: 0
Query Match: 34.74% Indels: 65
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US-10-659-782A-32 (1-116) x AX154581 (1-351)
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Db 108 ----- 108

QY 61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
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QY 81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100
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Db 108 ----- 108

QY 101 Arg-GluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
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Db 109 CAGAGAAAGGAGTCGAGAGAACCCAGCCAGCAGCTGCAGCCCGAGCTC 157

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GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 10, 2005, 07:58:59 ; Search time 407 Seconds
(without alignments)
1496.149 Million cell updates/sec

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Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 3	605.5	98.3	5036	4 AAK82033	Human inn
C 4	605.5	98.3	5036	4 AAK82030	Human inn
C 5	605.5	98.3	5036	5 ABA16827	Human ner
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ALIGNMENTS																
RESULT 1																
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XX																
AC	AAK82034;															
XX																
DT	07-NOV-2001	(first entry)														
XX																
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XX																
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KW	cytostatic; gene therapy; vaccine; metast															
XX																
OS	Homo sapiens.															
XX																
PN	WO200157182-A2.															
XX																
PD	09-AUG-2001.															
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PF	17-JAN-2001; 2001WO-US001354.															
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PR	31-JAN-2000; 2000US-0179065P.															
PR	04-FEB-2000; 2000US-0180628P.															
PR	24-FEB-2000; 2000US-0184664P.															
PR	02-MAR-2000; 2000US-0186350P.															
PR	16-MAR-2000; 2000US-0189874P.															
PR	17-MAR-2000; 2000US-0190076P.															
PR	18-APR-2000; 2000US-0198123P.															
PR	19-MAY-2000; 2000US-0205515P.															
PR	07-JUN-2000; 2000US-0209467P.															

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19	214	34.7	519	4	AAI59832	Aai59832 Human pol
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 PR 07-JUL-2000; 2000US-0216647P.
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 PR 11-JUL-2000; 2000US-0217487P.
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 PR 14-JUL-2000; 2000US-0218290P.
 PR 26-JUL-2000; 2000US-0220963P.
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 PR 14-AUG-2000; 2000US-0224518P.
 PR 14-AUG-2000; 2000US-0224519P.
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 PR 14-AUG-2000; 2000US-0225757P.
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 PR 23-AUG-2000; 2000US-0227009P.
 PR 30-AUG-2000; 2000US-0228924P.
 PR 01-SEP-2000; 2000US-0229287P.
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 PR 06-SEP-2000; 2000US-0230437P.
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 PR 08-SEP-2000; 2000US-0232081P.
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 PR 14-SEP-2000; 2000US-0232397P.
 PR 14-SEP-2000; 2000US-0232398P.
 PR 14-SEP-2000; 2000US-0232399P.
 PR 14-SEP-2000; 2000US-0232400P.
 PR 14-SEP-2000; 2000US-0232401P.
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 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.

(HUMA-) HUMAN GENOME SCI INC.
 Rosen CA, Barash SC, Ruben SM;
 WPI; 2001-483426/52.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 useful for preventing, diagnosing and/or treating cancers and metastasis.
 Disclosure; SEQ ID NO 36846; 3071pp + Sequence Listing; English.
 AA54951 to AA64702 encode the human immune/hematopoietic antigen (I)
 amino acid sequences given in AA82170 to AA91921. (I) have cytostatic
 activity, and can be used in gene therapy and vaccine production. (I)
 proteins and polynucleotides may be used in the prevention, diagnosis and
 treatment of diseases associated with inappropriate (I) expression. For
 example, they may be used to treat disorders associated with decreased
 expression by rectifying mutations or deletions in a patient's genome

CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patients own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting the
 CC nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/haematopoietic-related diseases, especially
 CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/haematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
 CC represent sequences used in the exemplification of the present invention
 XX
 SQ Sequence 5034 BP; 1049 A; 1324 C; 1291 G; 1370 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 3.33e-53 Length: 5034
 Score: 605.50 Matches: 116
 Percent Similarity: 99.15% Conservative: 0
 Best Local Similarity: 99.15% Mismatches: 0
 Query Match: 98.30% Indels: 1
 DB: 4 Gaps: 1

US-10-659-782A-32 (1-116) x AAK82034 (1-5034)

QY	1	MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu	20
DB	5034	ATGCCCTCCCGAGGACCTCTGCAGCCCTCTCTCGCATGCTCTGGCTGGACTTG	4975
QY	21	AlaMetAlaGlySerPheLeuSerProGluHisGlnArgValGlnValArgProPro	40
DB	4974	GCCATGGGAGGCTCCAGCTTCCTGAGCCCTGACACACAGAGTCCAGGTGAGACTCC	4915
QY	41	HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu	60
DB	4914	CACAAAGCCCAACATGTTGTTCCAGCCCTGCCACTTAGCAACAGCTCTGTGACCTGGAG	4855
QY	61	GlnGlnArgHis---TrpIleSerValPheSerGlnSerThrIysAspSerGlySerAsp	79
DB	4854	CAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCAGAGCACAAAGGACTCTGGGTCTGAC	4795
QY	80	LeuThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSer	99
DB	4794	CTCAGTGTTCGGAAGGACATGGGGGCTTAGAGTCTTAAACAGACTGTTCCCTCTCC	4735
QY	100	SerArgGluArgSerArgArgSerHisGlnProSerCysSerProGluLeu	116
DB	4734	AGCAGAGAAAGGAGTCTGAAGAGCCACCAAGCTGCAGCCCGAGCTC	4684

RESULT 2
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 XX
 AC ABA16829;
 XX
 DT 23-JAN-2002 (first entry)
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 DE Human nervous system related polynucleotide SEQ ID NO 9160.
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 KW Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
 KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnery;
 KW antiparkinsonian; antiskinking; antianaemic; antiarthritis; cancer;
 KW antihypertensive; hepatotropic; cerebroprotective; antiinflammatory;
 KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
 KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200159063-A2.
 XX
 XX 16-AUG-2001.
 PD
 XX 17-JAN-2001; 2001WO-US001334.
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PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX (HUMA-) HUMAN GENOME SCI INC.
PA Rosen CA, Barash SC, Ruben SM;
PI
XX

DR WPI; 2001-483426/52.
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and metastasis.
XX
PS Disclosure; SEQ ID NO 36845; 3071pp + Sequence Listing; English.
XX
CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 5036 BP; 1049 A; 1323 C; 1293 G; 1371 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3,336-53 Length: 5036
Score: 605.50 Matches: 116
Percent Similarity: 99.15% Conservative: 0
Best Local Similarity: 99.15% Mismatches: 0
Query Match: 98.30% Indels: 1
DB: 4 Gaps: 1

US-10-659-782A-32 (1-116) x AAK82033 (1-5036)

QY 1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
DB 5036 ATGCCCTCCCCAGGACCGTCTGCAGCCTCTGCTCTCCGCGATGCTCTGGCTGGACTTG 4977

QY 21 AlaMetAlaGlySerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
DB 4976 GCATGGCAGGCTCCAGCTTCTTGAGCCTGACACCGAGAGTCCAGTGACCTCC 4917

QY 41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
DB 4916 CACAAGGCCCACTATGTTGTTCCAGCCTGCCACTAGCAACAGCTCTGTGACCTGGAG 4857

QY 61 GlnGlnArgHis---TrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAsp 79
DB 4856 CAGCAGCGCCATCTCTGGGCTTTCAGTCTTCTCCAGAGCACAAAGGACTCTGGGCTGAC 4797

QY 80 LeuThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProSer 99
DB 4796 CTCACGTGTTCTGGAGGACATGGGGCTTAGAGTCTTAACAGACTGTTTCCCCCTTCC 4737

QY 100 SerArgGluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
DB 4736 AGCAGAGAAAGGATCGAAGAGCCACAGCCCAAGCTGAGCCCGGAGCTC 4686

RESULT 4
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AC AAK82030;
XX
DT -07-NOV-2001 (first entry)
XX
DE Human immune/hematopoietic antigen genomic sequence SEQ ID NO:36842.
XX
KW Human; immune; hematopoietic; immune/hematopoietic antigen; cancer;
KW Cytostatic; gene therapy; vaccine; metastasis; ds.

XX
OS Homo sapiens.
XX
PW WO200157182-A2.
XX
PD 09-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US001354.
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XX 31-JAN-2000; 2000US-0179065P.
XX 04-FEB-2000; 2000US-0180628P.
XX 24-FEB-2000; 2000US-0184664P.
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XX

PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and metastasis.
XX
XX Disclosure; SEQ ID NO 36842; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention
XX
XX Sequence 5036 BP; 1050 A; 1324 C; 1293 G; 1369 T; 0 U; 0 Other;
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Alignment Scores:
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Score: 605.50 Matches: 116
Percent Similarity: 99.15% Conservative: 0
Best Local Similarity: 99.15% Mismatches: 0
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QY 41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
Db 4916 CACAAAGCCCAACATGTTGTTCCAGCCCTGCCACTTAGCAACACAGCTCTGTGACCTGGAG 4857
QY 61 GlnGlnArgHis---TrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAsp 79
Db 4856 CAGCAGCGCCATCTCTGGGCTTTCAGTCTTCTCCAGAGCACAAAGGACTCTGGGTCTGAC 4797
QY 80 LeuThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSer 99
Db 4796 CTCACGTGTTCTGGAAGGACATGGGGGCTTAGAGTCTTAAACAGACTGTTCCTCCCTTCC 4737
QY 100 SerArgGluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
Db 4736 AGCAGAGAAAGGAGTCCGAAGAAGCCACCCAGCTGCAGCCCGCAGGCTC 4686

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ID ABA16827 standard; DNA; 5036 BP.
XX
AC ABA16827;
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XX 23-JAN-2002 (first entry)
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DE Human nervous system related polynucleotide SEQ ID NO 9158.
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KW Human; neurotropic; neuroprotective; cytostatic; dermatological; virucide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
KW antiparkinsonian; antispasmodic; antianaemic; antiarthritic; cancer;
KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
XX
OS Homo sapiens.
XX
PN WO200159063-A2.
XX
PD 16-AUG-2001.
XX
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XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-541565/60.
XX
XX Nucleic acids encoding 3224 human nervous system antigen polypeptides,
PT useful for preventing, diagnosing and/or treating nervous system cancers
PT and metastases.
XX
XX Disclosure; SEQ ID NO 9158; 1701pp + Sequence Listing; English.
XX
XX The invention relates to novel genes (ABA11004-ABA21534) and proteins
CC (AB14678-AB18001) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
CC infectious diseases such as viral, bacterial, fungal and parasitic
CC infections. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 5036 BP; 1050 A; 1324 C; 1293 G; 1369 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3,33e-53 Length: 5036
Score: 605.50 Matches: 116
Percent Similarity: 99.15% Conservative: 0
Best Local Similarity: 99.15% Mismatches: 0
Query Match: 98.30% Indels: 1
DB: 5 Gaps: 1

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QY 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
DB 4976 GCCATGGCAGGCTCCAGCTTCTCTGAGCCCTGACACACAGAGAGTCCAGGTGAGACCTCCC 4917

QY 41 HisLysAlaProHisValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
DB 4916 CACAAAGCCCAACATGTTGTTCCAGCCCTGACCAACAGAGTCCAGGTGAGACCTCCC 4857

QY 61 GlnGlnArgHis--TrpAlaSerValPheSerGlnSerThrIysAspSerGlySerAsp 79
DB 4856 CAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCAGAGCACAAAGGACTCTGGTCTGAC 4797

QY 80 LeuThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSer 99
DB 4796 CTCACGTGTTCTCGAAGGACATGGGGCTTAGAGTCTCTAAACAGACTGTTTCCCTCCCTCC 4737

QY 100 SerArgGluArgSerArgSerHisGlnProSerCysSerProGluLeu 116
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XX AC ABA16828;
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XX DT 23-JAN-2002 (first entry)
XX
XX DE Human nervous system related polynucleotide SEQ ID NO 9159.
XX
XX KW Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnery;
KW antiparkinsonian; antickling; antianaemic; antiarthritic; cancer;
KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW antiallergic; antidiabetic; antilicer; anticonvulsant; antifungal;
KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
XX
XX OS Homo sapiens.
XX
XX PN WO200159063-A2.
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XX PD 16-AUG-2001.
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XX PF 17-JAN-2001; 2001WO-US001334.
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 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 02-OCT-2000; 2000US-0237040P.
 PR 13-OCT-2000; 2000US-0239933P.
 PR 13-OCT-2000; 2000US-0239937P.
 PR 20-OCT-2000; 2000US-0240960P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241786P.
 PR 20-OCT-2000; 2000US-0241787P.
 PR 20-OCT-2000; 2000US-0241788P.
 PR 20-OCT-2000; 2000US-0241808P.
 PR 20-OCT-2000; 2000US-0241809P.
 PR 20-OCT-2000; 2000US-0241826P.
 PR 20-OCT-2000; 2000US-0242221P.
 PR 01-NOV-2000; 2000US-0244617P.
 PR 08-NOV-2000; 2000US-0244647P.
 PR 08-NOV-2000; 2000US-024475P.
 PR 08-NOV-2000; 2000US-024475P.
 PR 08-NOV-2000; 2000US-024476P.
 PR 08-NOV-2000; 2000US-024477P.
 PR 08-NOV-2000; 2000US-024478P.
 PR 08-NOV-2000; 2000US-024523P.
 PR 08-NOV-2000; 2000US-024524P.
 PR 08-NOV-2000; 2000US-024525P.
 PR 08-NOV-2000; 2000US-024525P.
 PR 08-NOV-2000; 2000US-024526P.
 PR 08-NOV-2000; 2000US-024527P.
 PR 08-NOV-2000; 2000US-024528P.
 PR 08-NOV-2000; 2000US-024532P.
 PR 08-NOV-2000; 2000US-024532P.
 PR 08-NOV-2000; 2000US-024609P.
 PR 08-NOV-2000; 2000US-024610P.
 PR 08-NOV-2000; 2000US-024611P.
 PR 08-NOV-2000; 2000US-024613P.
 PR 17-NOV-2000; 2000US-0249207P.
 PR 17-NOV-2000; 2000US-0249208P.
 PR 17-NOV-2000; 2000US-0249209P.
 PR 17-NOV-2000; 2000US-0249210P.
 PR 17-NOV-2000; 2000US-0249211P.
 PR 17-NOV-2000; 2000US-0249212P.
 PR 17-NOV-2000; 2000US-0249213P.
 PR 17-NOV-2000; 2000US-0249214P.
 PR 17-NOV-2000; 2000US-0249215P.
 PR 17-NOV-2000; 2000US-0249216P.
 PR 17-NOV-2000; 2000US-0249217P.
 PR 17-NOV-2000; 2000US-0249218P.
 PR 17-NOV-2000; 2000US-0249244P.
 PR 17-NOV-2000; 2000US-0249245P.

PR 17-NOV-2000; 2000US-0249264P.
 PR 17-NOV-2000; 2000US-0249265P.
 PR 17-NOV-2000; 2000US-0249297P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 17-NOV-2000; 2000US-0249300P.
 PR 01-DEC-2000; 2000US-0250391P.
 PR 01-DEC-2000; 2000US-0251160P.
 PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0256719P.
 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-541565/60.
 XX
 DR Nucleic acids encoding 3224 human nervous system antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating nervous system cancers
 PT and metastases.
 XX
 PS Disclosure; SEQ ID NO 9159; 1701pp + Sequence Listing; English.
 XX
 CC The invention relates to novel genes (ABA11004-ABA21534) and proteins
 CC (ABB14678-ABB18001) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
 CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
 CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
 CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
 CC cardiovascular disorders such as myocardial ischaemia; (d) wound healing
 CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
 CC infectious diseases such as viral, bacterial, fungal and parasitic
 CC infections. Note: the sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 5036 BP; 1049 A; 1323 C; 1293 G; 1371 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 3.33e-53 Length: 5036
 Score: 605.50 Matches: 116
 Percent Similarity: 99.15% Conservativity: 0
 Best Local Similarity: 99.15% Mismatches: 0
 Query Match: 98.30% Indels: 1
 DB: 5 Gaps: 1
 US-10-659-782A-32 (1-116) x ABA16828 (1-5036)
 QY 1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTriLeuAspLeu 20
 |||||
 Db 5036 ATGCCCTCCCGAGGACCGCTCTGCAGCCTCTGCTCTCGCATGCTCTGCTGACTTG 4977
 QY 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
 |||||
 Db 4976 GCCATGGCAGGCTCCAGCTTCTGAGCCCTGAACACACAGAGAGTCCAGGTGAGACCTCCC 4917
 QY 41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
 |||||
 Db 4916 CACAAAGCCCCACATGTTGTTCCAGCCCTGCCACTTAGCAACCACTCTGTGACCTGGAG 4857

PN WO9842840-A1.
XX PD 01-OCT-1998.
XX PF 23-MAR-1998; 98WO-US005620.
XX PR 24-MAR-1997; 97US-0041102P.
XX PR 24-MAR-1997; 97US-00822897.
XX PA (ZYMO) ZYMOGENETICS INC.
XX PI Sheppard PO, Deisher TA;
XX WPI; 1999-070071/06.
XX DR P-PSDB; AAW87991.
XX
PT Human polypeptide having homology to motilin, zsig33 - useful e.g. to
PT treat gastrointestinal motility disorders, obesity etc. and to identify
PT antagonists to treat gastrointestinal hypermotility.
XX
XX PS Claim 5; Page 54-55; 69pp; English.
XX
CC The present sequence encodes a protein designated Zsig33. The nucleic
CC acids are strongly expressed in stomach tissue. The polypeptide (or
CC allelic variants/orthologs) can be used to stimulate gastric motility,
CC measured as increased transit time or gastric emptying of an ingested
CC substance in mammals. The products are used to treat disorders associated
CC with gastrointestinal cell contractility, secretion of digestive
CC enzymes/acids, gastrointestinal motility, recruitment of digestive
CC enzymes, gastrointestinal inflammation, reflux disease and nutrient
CC absorption regulation. Zsig33 polypeptides may also be important
CC neurologically, since the family of gut-brain peptides to which the
CC homologous protein motilin belongs has been associated with neurological
CC and CNS functions. They may therefore be used e.g. to regulate satiety or
CC treat obesity and other metabolic disorders where neurological feedback
CC modulates nutritional absorption. They are useful to identify zsig33
CC agonists, antagonists and ligands and to produce antibodies
XX
SQ Sequence 351 BP; 82 A; 107 C; 107 G; 55 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1,84e-13 Length: 351
Score: 214.00 Matches: 51
Percent Similarity: 44.44% Conservatives: 1
Best Local Similarity: 43.59% Mismatches: 0
Query Match: 34.74% Indels: 65
DB: 2 Gaps: 1

US-10-659-782A-32 (1-116) x AAX04550 (1-351)
QY 1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
Db 1 ATGCCCTCCCGAGGACCGTCTCGAGCTCTCTCGCATCTCTGGCTGGACTTG 60
QY 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
Db 61 GCCATGGCAGGCTCCAGCTCTCTGAGCCCTGAACACAGAGAGTCCAG----- 108
QY 41 HisLysAlaProHisValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
Db 108 ----- 108
QY 61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
Db 108 ----- 108
QY 81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProSerSer 100
Db 108 ----- 108
QY 101 Arg-GluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
Db 109 CAGAGNAGAGAGTTCGAGNAGAGCCACGACGACGAGCTGACGCCCGAGCTC 157

RESULT 9
AAF30033 standard; DNA; 351 BP.
XX AAF30033;
XX AC AAF30033;
XX DT 23-APR-2001 (first entry)
XX DE DNA encoding zsig33.
XX SGIP; zsig33; human; chromosome 3p26.1; anorectic; antidiabetic;
XX KW nutritional absorption modulator; growth hormone secretagogue;
XX KW somatotropin; somatostatin-C; gene therapy; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT sig_peptide 1..69
FT mat_peptide /*tag= a
FT 70..351 /*tag= b
XX WO200100830-A1.
XX PD 04-JAN-2001.
XX PF 30-JUN-2000; 2000WO-US018306.
XX PR 30-JUN-1999; 99US-00345157.
XX (ZYMO) ZYMOGENETICS INC.
XX Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
XX WPI; 2001-123010/13.
XX DR P-PSDB; AAB20101.
XX Novel variants of SGIP peptides for modulating contractility in duodenum
XX or jejunum tissue, pancreatic secretion of hormones and digestive
XX enzymes, inducing growth hormone secretion or modulating gastric
XX emptying.
XX PS Disclosure; 54; 61pp; English.
XX The present sequence is that of DNA encoding zsig33 (see AAB20101), a
XX secreted protein with homology to motilin (see AAB20102). Human zsig33 is
XX expressed at high levels in the stomach, and at lower levels in the small
XX intestine and pancreas. A novel peptide fragment of zsig33, termed SGIP
XX (see AAB20100), is claimed. SGIP is a ligand for growth hormone
XX secretagogue receptor, and is therefore useful for modulating secretion
XX of growth hormone and insulin like growth factor 1. SGIP, and variant
XX SGIP peptides, are used in claimed methods for stimulating
XX contractility in duodenum or jejunum tissue, modulating pancreatic
XX secretion of hormones and digestive enzymes, inducing growth hormone
XX secretion, and modulating gastric emptying
XX
SQ Sequence 351 BP; 82 A; 107 C; 107 G; 55 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1,84e-13 Length: 351
Score: 214.00 Matches: 51
Percent Similarity: 44.44% Conservatives: 1
Best Local Similarity: 43.59% Mismatches: 0
Query Match: 34.74% Indels: 65
DB: 4 Gaps: 1

US-10-659-782A-32 (1-116) x AAF30033 (1-351)
QY 1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
Db 1 ATGCCCTCCCGAGGACCGTCTCGAGCTCTCTCGCATCTCTGGCTGGACTTG 60

QY 21 AlaMetAlaGlySerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
 Db 61 GCCATGCGAGCTCCAGCTTCCTGAGCCCTGAACACCCAGAGAGTCCAG----- 108
 QY 41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
 Db 108 ----- 108
 QY 61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
 Db 108 ----- 108
 QY 81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100
 Db 108 ----- 108
 QY 101 Arg-GluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
 Db 109 CAGAGAAGAGGTCGAAGAAGCCACCCAGCCAGCTGACGCCCGAGCTC 157

RESULT 10

AAF83678
 ID AAF83678 standard; cDNA; 351 BP.
 XX
 AC AAF83678;

23-JUL-2001 (first entry)

Human zsig33 polypeptide encoding cDNA.

zsig33; signal transduction; hormone; enzyme; neural development;
 gastric contractility; nutrient uptake; digestive; pancreatic; human;
 insulin-like growth factor-I; growth hormone; bone; gastrointestinal;
 glucose; osteopathic; anorectic; vulnery; immunomodulator; GHS-R;
 G-protein coupled receptor; ss.

OS Homo sapiens.

Key Location/Qualifiers

FT CDS 1..351
 FT /tag= a
 FT /product= "zsig33"
 FT /note= "the stop codon is not indicated"

WO200138355-A2.

31-MAY-2001.

22-NOV-2000; 2000WO-US032074.

22-NOV-1999; 99US-0166765P.

(ZYMO) ZYMOGENETICS INC.

Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;

WPI; 2001-355879/37.

P-PSDB; AAB62649.

Forming reversible peptide receptor complex for purifying cell and
 peptides, stimulating signal transduction and modulating hormone
 secretion, involves contacting a receptor with zsig33 polypeptide.

Example 2; Page 93-94; 11lpp; English.

The invention relates to a method of forming a reversible peptide-
 receptor complex that involves providing an immobilized receptor, and
 contacting the receptor with a zsig33 peptide (comprising residues 24-37
 of AAB62649), where the receptor binds to the zsig33 peptide. The method
 is useful for purifying cells, purifying a peptide, stimulating signal
 transduction in a cell expressing a receptor. It is also useful for
 modulating secretion of hormones, neural development and/or utilization,
 gastric contractility, nutrient uptake, secretion of digestive and

CC pancreatic enzymes and hormones, secretion of insulin-like growth factor
 CC -I, secretion of non-zsig33 proteins. It is useful for modulating growth
 CC hormone secretion in a mammal having a disease associated with abnormal
 CC levels of growth hormone, such as osteoporosis, bone repair, bone
 CC remodeling, low osteoblast levels, cartilage repair and remodeling,
 CC skeletal dysplasia, immune suppression, obesity, growth retardation,
 CC protein catabolic responses after surgery, cachexia, protein loss,
 CC dwarfism, wound healing and ovulation induction, treating a mammal
 CC a metabolic disorder requiring neurological feedback, such as satiety
 CC regulation, glucose absorption and metabolism and neuropathy-associated
 CC gastrointestinal disorders, and stimulating glucose-induced insulin
 CC release in a mammal. The present sequence represents the cDNA encoding
 CC the human zsig33 polypeptide, a peptide ligand for the G-protein coupled
 CC receptor, GHS-R
 XX

SQ Sequence 351 BP; 82 A; 107 C; 107 G; 55 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.84e-13 Length: 351
 Score: 214.00 Matches: 51
 Percent Similarity: 44.44% Conservative: 1
 Best Local Similarity: 43.59% Mismatches: 0
 Query Match: 34.74% Indels: 65
 DB: 4 Gaps: 1

US-10-659-782A-32 (1-116) x AAF83678 (1-351)

QY 1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
 Db 1 ATGCCCTCCCGAGGACCGCTGCGAGCTCTCGGCATGCTCTGGCTGGAGCTTG 60
 QY 21 AlaMetAlaGlySerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
 Db 61 GCCATGCGAGCTCCAGCTTCCTGAGCCCTGAACACCCAGAGAGTCCAG----- 108
 QY 41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
 Db 108 ----- 108
 QY 61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
 Db 108 ----- 108
 QY 81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100
 Db 108 ----- 108
 QY 101 Arg-GluArgSerArgArgSerHisGlnProSerCysSerProGluLeu.116
 Db 109 CAGAGAAGAGGTCGAAGAAGCCACCCAGCCAGCTGACGCCCGAGCTC 157

RESULT 11

ABV72214
 ID ABV72214 standard; DNA; 351 BP.
 XX
 AC ABV72214;

05-DEC-2002 (first entry)

Nucleotide sequence of a human zsig33.

Short gastrointestinal peptide; SGIP; zsig33; motilin; gene; ss.

OS Homo sapiens.

Key Location/Qualifiers
 FT CDS 1..351
 FT /tag= a
 FT /product= "zsig33"
 FT /note= "no termination codon given"
 FT sig_peptide 1..69
 FT /tag= b
 FT mat_peptide 70..3510

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FT      /*tag= c
XX      US6420521-B1.
XX      PD      16-JUL-2002.
XX      PF      30-JUN-2000; 2000US-00608810.
XX      PR      30-JUN-1999; 99US-0141592P.
XX      PA      (ZYMO ) ZYMOGENETICS INC.
XX      XX      Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
XX      WPI; 2002-634794/68.
XX      DR      P-PSDB; ABB78319.
XX      PT      New Short Gastrointestinal Peptide, which has homology to motilin, useful
XX      PT      for preventing, diagnosing and treating gastrointestinal disorders.
XX      PS      Disclosure; Col 37-40; 23pp; English.
XX      CC      The present sequence encodes human zsig33. The specification describes a
XX      CC      short gastrointestinal peptide (SGIP), which is derived from zsig33. SGIP
XX      CC      has homology to motilin. The SGIP peptide may be used in the prevention,
XX      CC      diagnosis and treatment of diseases associated with inappropriate SGIP
XX      CC      expression. For example, SGIP may be used to treat disorders associated
XX      CC      with decreased expression by rectifying mutations or deletions in a
XX      CC      patient's genome that affect the activity of SGIP by expressing inactive
XX      CC      proteins or to supplement the patient's own production of SGIP. SGIP may
XX      CC      also be used as an antigen in the production of antibodies against SGIP
XX      CC      and in assays to identify modulators of SGIP expression and activity. The
XX      CC      anti-SGIP antibodies, agonists and antagonists may also be used to
XX      CC      regulate expression and activity. The anti-SGIP antibodies may also be
XX      CC      used as diagnostic agents for detecting the presence of SGIP in samples
XX      SQ      Sequence 351 BP; 82 A; 107 C; 107 G; 55 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      1.84e-13      Length:      351
Score:      214.00      Matches:      51
Percent Similarity:      44.4%      Conservative:      1
Best Local Similarity:      43.5%      Mismatches:      0
Query Match:      34.7%      Indels:      65
DB:      Gaps:      1

US-10-659-782A-32 (1-116) x ABV72214 (1-351)

QY      1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
DB      1 ATGCCCTCCCGAGGACCGTCTGCAGCTCTCGCTCCGCGATGCTCTGGCTGGACTTG 60
QY      21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
DB      61 GCCATGGCAGGCTCCAGCTTCTGAGCCTCTGACACCGAGAGTCCAG----- 108
QY      41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
DB      108 ----- 108
QY      61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
DB      108 ----- 108
QY      81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProSerSer 100
DB      108 ----- 108
QY      101 Arg-GluArgSerArgSerHisGlnProSerCysSerProGluLeu 116
DB      109 CAGAGAAAGGAGTCAAGGAAGCCACGACGACGAGCTGCAGCCCGAGCTC 157

RESULT 12

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```

AD133327
ID      AD133327 standard; cDNA; 351 BP.
XX
AC      AD133327;
XX
DT      22-APR-2004 (first entry)
XX
DE      Motilin homologous Zsig33 protein encoding DNA.
XX
KW      motilin; secretin gastric inhibitory peptide; SGIP; contractility;
KW      duodenum; jejunum; pancreatic secretion; hormone; digestive enzyme;
KW      growth hormone secretion; gastric emptying; gene; ss; human.
XX
OS      Homo sapiens.
XX
FH      Key      Location/Qualifiers
CDS      1..351
FT      /*tag= a
XX
PN      US2003176640-A1.
XX
PD      18-SEP-2003.
XX
PF      01-JUL-2002; 2002US-00186414.
XX
PR      30-JUN-1999; 99US-0141592P.
PR      30-JUN-2000; 2000US-00608810.
XX
PA      (ZYMO ) ZYMOGENETICS INC.
XX
PI      Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;
XX
WPI; 2003-898590/82.
DR      P-PSDB; AD133328.
XX
PT      New secretin gastric inhibitory peptides (SGIP), useful for modulating
PT      contractility in duodenum or jejunum tissue, the pancreatic secretion of
PT      hormones and digestive enzymes, or gastric emptying, inducing growth
PT      hormone secretion.
XX
XX      Disclosure; SEQ ID NO 3; 26pp; English.
XX
XX      The invention relates to novel polynucleotides, polypeptides, peptides,
XX      variants and used thereof for peptide fragments which have homology to
XX      motilin. The invention further provides agonists, variants, antibodies,
XX      and host cells expressing the cDNA encoding the novel secretin gastric
XX      inhibitory peptide (SGIP). The invention further relates to: modulating
XX      contractility in duodenum or jejunum tissue by administering the isolated
XX      polypeptide to the tissue; modulating the pancreatic secretion of
XX      hormones and digestive enzymes by administering the isolated polypeptide
XX      to the mammal; inducing growth hormone secretion by administering the
XX      polypeptide to the mammal; modulating gastric emptying by administering the
XX      isolated polypeptide to the mammal. The polypeptide and methods are
XX      useful for modulating contractility in duodenum or jejunum tissue,
XX      modulating the pancreatic secretion of hormones and digestive enzymes,
XX      inducing growth hormone secretion, and modulating gastric emptying. This
XX      polynucleotide sequence represents the DNA encoding a motilin homologous
XX      Zsig33 protein of the invention.
XX
SQ      Sequence 351 BP; 82 A; 107 C; 107 G; 55 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      1.84e-13      Length:      351
Score:      214.00      Matches:      51
Percent Similarity:      44.4%      Conservative:      1
Best Local Similarity:      43.5%      Mismatches:      0
Query Match:      34.7%      Indels:      65
DB:      Gaps:      1

US-10-659-782A-32 (1-116) x AD133327 (1-351)

QY      1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20

```

Db 1 ATGCCCTCCAGGACCGTCTCGAGCCTCTCTCGCATGCTCTGGCTGGACTTG 60
 Qy 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
 Db 61 GCCATGCGAGGCTCCAGCTTCTGAGCCCTGAACACAGAGAGTCCAG----- 108
 Qy 41 HisLysAlaProHisValValProAlaLeuProLeuSerHisGlnLeuCysAspLeuGlu 60
 Db 108 ----- 108
 Qy 61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
 Db 108 ----- 108
 Qy 81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100
 Db 108 ----- 108
 Qy 101 Arg-GluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
 Db 109 CAGAGAAAGGAGTTCGAGAGAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCTC 157
 RESULT 13
 ADN11752
 ID ADN11752 standard; cDNA; 351 BP.
 AC ADN11752;
 XX
 XX 15-JUL-2004 (first entry)
 DT
 DE Human zsig33 coding sequence.
 XX
 KW ss; gene; human; zsig33; body weight; body mass; antibody; antagonist;
 KW gastrointestinal; antiinflammatory; antiulcer; vulnerary;
 KW growth hormone secretagogue; GHS-R; peptide-antibody complex.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..351
 FT /*tag= a
 FT /product= "zsig33"
 FT /partial
 FT /note= "no stop codon"
 XX
 PN WO2004033645-A2.
 XX
 PD 22-APR-2004.
 XX
 PF 06-OCT-2003; 2003WO-US031804.
 XX
 PR 07-OCT-2002; 2002US-0416918P.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Jaspers SR, Sheppard PO, Bishop PD, Kuijper JL, Deisher TA;
 XX
 DR WPI; 2004-340913/31.
 DR P-PSDB; ADN11753.
 XX
 XX Use of a zsig33 peptide for e.g. forming a peptide-antibody complex,
 PT inhibiting signal transduction in a cell expressing a growth hormone
 PT secretagogue receptor, or treating a metabolic disorder.
 XX
 PS Example 2; Page 88; 100pp; English.
 XX
 CC The present invention relates to the use of a zsig33 peptide for forming
 CC a peptide-antibody complex, purifying a peptide, inhibiting signal
 CC transduction in a cell expressing a growth hormone secretagogue receptor
 CC (GHS-R), decreasing fat deposition in a mammal, suppressing the appetite
 CC of a mammal, inhibiting growth hormone secretion in pituitary cells of a
 CC mammal, or treating a metabolic disorder. The peptide is useful for
 CC forming a peptide-antibody complex, purifying a peptide, inhibiting

CC signal transduction in a cell expressing a GHS-R, decreasing fat
 CC deposition in a mammal, suppressing the appetite of a mammal, inhibiting
 CC growth hormone secretion in pituitary cells of a mammal, or treating a
 CC metabolic disorder. The zsig33 polypeptides can be used to study
 CC proliferation or differentiation in stomach, lung, pituitary,
 CC hypothalamus, hippocampus, kidney, jejunum, small intestine,
 CC skeletal muscle or pancreas. They are also useful in delivering
 CC therapeutic agents. Zsig33 polypeptides, agonists and antagonists are
 CC also useful for promoting wound healing. The polypeptides, nucleic acids
 CC and antibodies are useful for diagnosing, treating or preventing
 CC disorders associated with gastric reflux, gastroparesis, modulation of
 CC secretion of pituitary hormones, including growth hormone, Crohn's
 CC disease, metabolic wasting, gastric ulcers, weight management, or
 CC degenerative disease. The present sequence is the human zsig33 coding
 CC sequence.
 XX
 SQ Sequence 351 BP; 82 A; 107 C; 107 G; 55 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.84e-13 Length: 351
 Score: 214.00 Matches: 51
 Percent Similarity: 44.44% Conservative: 1
 Best Local Similarity: 43.59% Mismatches: 0
 Query Match: 34.74% Indels: 65
 DB: 12 Gaps: 1

US-10-659-782A-32 (1-116) x ADN11752 (1-351)

Qy 1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
 Db 1 ATGCCCTCCAGGACCGTCTCGAGCCTCTCTCGCATGCTCTGGCTGGACTTG 60
 Qy 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
 Db 61 GCCATGCGAGGCTCCAGCTTCTGAGCCCTGAACACAGAGAGTCCAG----- 108
 Qy 41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
 Db 108 ----- 108
 Qy 61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
 Db 108 ----- 108
 Qy 81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100
 Db 108 ----- 108
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RESULT 14

AAD50726
 ID AAD50726 standard; DNA; 401 BP.
 XX
 AC AAD50726;
 XX
 DT 02-APR-2003 (first entry)
 XX
 DE Human exon 3-deleted ghrelin DNA.
 XX
 KW Ghrelin; preproghrelin; GHS-R 1b; benign prostatic hyperplasia; therapy;
 KW breast; cervical; uterine; choriocarcinoma; prostate; ovary; cytostatic;
 KW cancer; human; gene; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 33..308
 FT /*tag= a
 FT /product= "Human exon 3-deleted ghrelin protein"
 XX

PN WO200290387-A1.
 XX 14-NOV-2002.
 XX 10-MAY-2002; 2002WO-AU000582.
 XX 10-MAY-2001; 2001AU-00004919.
 PR 17-DEC-2001; 2001AU-00009567.
 XX (UYQU-) UNIV QUEENSLAND TECHNOLOGY.
 XX Chopin LK, Jeffery PL, Herington AC;
 PI WPI; 2003-111957/10.
 DR P-PSDB; AAB33410.
 XX Identifying a cancer cell or tissue for treating prostate, ovarian,
 PT breast cancer, or benign prostatic hyperplasia, by detecting the
 PT expression of a ghrelin, an exon-3 deleted preproghrelin and/or a GHS-R
 PT 1b proteins or nucleic acids.
 XX Example 1; Fig 1; 50pp; English.
 XX The invention relates to a method for identifying a cancer cell or tissue
 CC of the reproductive system by detecting expression of a ghrelin, an exon-
 CC 3 deleted preproghrelin and/or a GHS-R 1b proteins or nucleic acids. The
 CC antibodies, exon 3-deleted form of preproghrelin and antagonists are
 CC useful for treating cancer of the reproductive system such as prostate,
 CC ovarian, breast, cervical or uterine cancer, choriocarcinoma or benign
 CC prostatic hyperplasia. The present sequence is human exon 3-deleted
 CC ghrelin DNA
 XX
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 Score: 214.00 Matches: 51
 Percent Similarity: 44.44% Conservative: 1
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 QY 41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
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 QY 61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
 Db 140 ----- 140
 QY 81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100
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 Db 141 CAGAGAAGAGTTCGAGAAGACCCAGCAGCTGCACCCCGAGCTC 199
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 AAF59645
 ID AAF59645 standard; cDNA; 494 BP.
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 AC AAF59645;

XX 24-APR-2001 (first entry)
 DE Human ghrelin preproprotein cDNA, SEQ ID NO:7.
 XX Growth hormone secretagogue; GHS; ghrelin; precursor; preproprotein;
 KW calcium concentration elevation; infant growth disorder;
 KW growth hormone deficiency; ss.
 XX Homo sapiens.
 OS WO200107475-A1.
 PN 01-FEB-2001.
 PD 24-JUL-2000; 2000WO-JP004907.
 PF 23-JUL-1999; 99JP-00210002.
 PR 29-NOV-1999; 99JP-00338841.
 PR 26-APR-2000; 2000JP-00126623.
 XX (KANG/) KANGAWA K.
 PA Kangawa K, Kojima M, Hosoda H, Matsuo H, Minamitake Y;
 PI WPI; 2001-159704/16.
 DR P-PSDB; AAB60511.
 XX New peptide compounds which induce growth hormone secretion and elevate
 PT cell calcium concentrations, useful in treatment and diagnosis of infant
 PT growth disorders.
 XX Claim 42; Page 183-184; 210pp; Japanese.
 PS The invention relates to a novel peptide compound or its salt which
 CC induces the secretion of growth hormone and/or elevates calcium ion
 CC concentration in cells. The peptides are ghrelin homologues and are
 CC characterised in that at least one amino acid has been substituted by a
 CC modified amino acid and/or a non-amino acid compound. The invention also
 CC encompasses the unmodified peptides; the DNA encoding the peptides;
 CC vectors and host cells comprising such DNA; a method of producing the
 CC peptides comprising recombinant production, optionally followed by
 CC chemical modification; an antibody specific for a peptide of the
 CC invention; and an assay and kit for detecting the peptides. The peptides
 CC of the invention are useful for treating and/or diagnosing diseases
 CC caused by a deficiency in growth hormone expression or activity. In
 CC particular, they are useful for promoting infant growth due to growth
 CC hormone deficiency. The compounds of the invention are safe with no
 CC accompanying side effects. The present sequence represents cDNA encoding
 CC a ghrelin-type growth hormone secretagogue (GHS) precursor protein of the
 CC invention
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 Score: 214.00 Matches: 51
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 Best Local Similarity: 43.59% Mismatches: 0
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 QY 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgPro 40
 Db 94 GCCATGGCAGGCTCCAGCTTCTGAGCCCTGAACACACAGAGATCCAG----- 141
 QY 41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60

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Db      141 ----- 141
QY      61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
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Db      141 ----- 141
QY     101 Arg-GluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
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GenCore version 5.1.6
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Run on: February 10, 2005, 13:49:58 ; Search time 85 Seconds
(without alignments)
970.018 Million cell updates/sec

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Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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-DRV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPEXT=10 -XGAPEXT=0.5 -FGAPOB=6
-FGAPEXT=7 -YGAPOB=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	214	34.7	351	3	US-08-822-897C-1
3	214	34.7	351	4	US-09-608-810A-3
4	214	34.7	351	4	US-09-404-417A-1
5	214	34.7	654	4	US-10-140-002-441
6	91.5	14.9	9377	4	US-09-801-874-3
7	87	14.1	969	4	US-09-252-991A-12776
8	87	14.1	2266	2	US-09-213-767-1
9	85	13.8	536165	4	US-09-214-808-1
10	82.5	13.4	867	4	US-09-252-991A-13395
11	82.5	13.4	2103	4	US-09-252-991A-13604
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13	81.5	13.2	5367	3	US-08-976-255-2	Sequence 2, Appli
14	81	13.1	8285	4	US-09-732-025-3	Sequence 3, Appli
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17	79.5	12.9	539	4	US-09-270-767-1719	Sequence 1719, Ap
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19	79.5	12.9	2135	1	US-07-938-333A-3	Sequence 3, Appli
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21	79.5	12.9	5816	3	US-08-857-076-11	Sequence 11, Appl
22	79	12.8	652	3	US-08-998-416-962	Sequence 962, App
23	78.5	12.7	4403765	3	US-09-103-840A-2	Sequence 2, Appli
24	78.5	12.7	4411529	3	US-09-103-840A-1	Sequence 1, Appli
25	78	12.7	1500	4	US-09-489-039A-2848	Sequence 2848, Ap
26	78	12.7	1518	4	US-09-489-039A-2774	Sequence 2774, Ap
27	77.5	12.6	856	4	US-09-535-008-55	Sequence 55, Appl
28	77.5	12.6	34094	4	US-09-292-034-1	Sequence 1, Appli
29	77	12.5	864	4	US-09-252-991A-2337	Sequence 2337, Ap
30	77	12.5	2088	4	US-09-252-991A-2576	Sequence 2576, Ap
31	76.5	12.4	1020	4	US-09-252-991A-3809	Sequence 3809, Ap
32	76.5	12.4	1122	4	US-09-252-991A-3853	Sequence 3853, Ap
33	76.5	12.4	1197	4	US-10-037-616-8	Sequence 8, Appli
34	76	12.3	1504	2	US-08-839-008-4	Sequence 4, Appli
35	76	12.3	1506	2	US-08-839-008-6	Sequence 6, Appli
36	76	12.3	2374	3	US-09-347-801-3	Sequence 3, Appli
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38	75.5	12.3	2790	3	US-08-985-950-21	Sequence 21, Appl
39	75.5	12.3	2790	4	US-09-546-049-21	Sequence 21, Appl
40	75.5	12.3	2922	3	US-09-310-463-1	Sequence 1, Appli
41	75.5	12.3	2922	4	US-08-842-248A-1	Sequence 1, Appli
42	75.5	12.3	4748	4	US-08-426-630-29	Sequence 29, Appl
43	75	12.2	850	4	US-09-895-652A-6	Sequence 6, Appli
44	75	12.2	4286	3	US-09-413-304-7	Sequence 7, Appli
45	75	12.2	4286	4	US-09-817-856-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-046-479-1
; Sequence 1, Application US/09046479
; Patent No. 6231653
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Deisher, Theresa A.
; TITLE OF INVENTION: MOTILIN HOMOLOGS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,479
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:

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; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 351 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
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; NAME/KEY: Coding Sequence
; LOCATION: 1...351
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; NAME/KEY: sig_peptide
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; LOCATION: 70...351
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QY 41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
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QY 81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100
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RESULT 2
US-08-822-897C-1
; Sequence 1, Application US/08822897C
; Patent No. 6380158
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Deisher, Theresa A.
; TITLE OF INVENTION: MOTILIN HOMOLOGS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; .COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/822,897C
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
;
INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 351 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
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; LOCATION: 1...351
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DB 61 GCCATGGCAGGCTCCAGCTTCTGAGCCCTGAACACACAGAGAGTCCAG----- 108
QY 41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
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QY 81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100
DB 108 ----- 108
QY 101 Arg-GluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
DB 109 CAGAGAAAGGAGTCCGAGAGCCACCCAGCTGACAGCTGACCCCGAGCTC 157

RESULT 3
US-09-608-810A-3
; Sequence 3, Application US/09608810A
; Patent No. 6420521
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; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Jaepers, Stephen R.
; APPLICANT: Deisher, Theresa A.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: SGIP PEPTIDES
; FILE REFERENCE: 99-51
; CURRENT APPLICATION NUMBER: US/09/608,810A
; PRIOR FILING DATE: 2000-06-30
; CURRENT FILING DATE: 2002-05-06
; NUMBER OF SEQ ID NOS: 7
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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
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; TYPE: DNA
; ORGANISM: Homo sapiens
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; NAME/KEY: CDS
; LOCATION: (1)...(351)
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; LOCATION: (70)...(351)
US-09-608-810A-3

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Pred. No.: 5,14e-17 Length: 351
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QY 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
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QY 41 HisLysAlaProHisValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
DB 108 ----- 108
QY 61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
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QY 81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProSerSer 100
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; Patent No. 662729
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Deisher, Theresa A.
; APPLICANT: Jaepers, Stephen R.
; TITLE OF INVENTION: TML PEPTIDES
; FILE REFERENCE: 97-04CI
; CURRENT APPLICATION NUMBER: US/09/404,417A
; CURRENT FILING DATE: 1999-09-23
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RESULT 5
US-10-140-002-441
; Sequence 441, Application US/10140002
; Patent No. 6725730
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C59
; CURRENT APPLICATION NUMBER: US/10/140,002
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550

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 Db 160 CTGAACAGACCACTTCCACCGACTCTGCTCACTCACTGCTATATACGCGGTACGATC 101
 QY 104 SerArgArgSerHisGlnProSerCysSer 113
 Db 100 GAGTTCGTCGACATCAAGAGCTGTAGC 71

RESULT 8

US-09-213-767-1
 ; Sequence 1, Application US/09213767
 ; Patent No. 5948680
 ; GENERAL INFORMATION:
 ; APPLICANT: Brenda F. Baker
 ; APPLICANT: Lex M. Cowsett
 ; FILE OF INVENTION: ANTISENSE MODULATION OF ELK-1 EXPRESSION
 ; FILE REFERENCE: RTS-0024
 ; CURRENT APPLICATION NUMBER: US/09/213,767
 ; CURRENT FILING DATE: 1998-12-17
 ; NUMBER OF SEQ ID NOS: 47
 ; SEQ ID NO 1
 ; LENGTH: 2266
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (316)..(1602)

US-09-213-767-1

Alignment Scores:
 Pred. No.: 1.82 Length: 2266
 Score: 87.00 Matches: 41
 Percent Similarity: 35.86% Conservative: 11
 Best Local Similarity: 28.28% Mismatches: 47
 Query Match: 14.12% Indels: 46
 DB: 2 Gaps: 8

US-10-659-782A-32 (1-116) x US-09-213-767-1 (1-2266)

QY 2 ProSerProGlyThrValCysSerLeu-----LeuLeuLeuGlyMetLeuTrpLeu 18
 Db 797 CTTTCACCATCAGTCTGCGAGCGCAGCCACCCCTTCATCTCGGCTGCTGTGG--- 853
 QY 19 AspLeuAlaMetAlaGlySerSerPheLeuSerPro---GluHisGlnArgValGlnVal 37
 Db 854 -----TGCTCCCAATGCAGCTCTCTGAGGGGCGAGCAG 886
 QY 38 ArgProProHisLysAlaProHisValVal-----ProAlaLeuProLeu 52
 Db 887 CGCCCTCCCTCGGGGAGAGGAGCACCAGTCCAAAGCCCTTGGAGGCCCTGCTCGAGGCTG 946
 QY 53 SerAsnGlnLeuCys-----TGCTCCCAATGCAGCTCTCTGAGGGGCGAGCAG 57
 Db 947 AAGAGCGCGCTTGCTCTGAGGTGATCTGACCCCGCCGAGCGCCCAACCTGAAT 1006
 QY 58 -----AspLeuGluGlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAsp 75
 Db 1007 CGGAAGAGCTTAATGTGGAGCGGGTTGGGCGGGCTTGGCCCGCAGAAAGTAAAGTAG 1066
 QY 76 SerGlySerAspLeuThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeu 95
 Db 1067 AAGGGC-----CCAAAGGAAGAGTTCGAGGAGGAGAGAGGGTTG 1111
 QY 96 PhePro-----ProSerArgGluArgSerArgArgSerHisGlnProSer 111
 Db 1112 TCACGAACACCAAGCCGAGCAGAGTCCCTCCACAGAGGGCGTGCAGCCCGCG 1171
 QY 112 CysSerProGluLeu 116

Db 1172 TGC---CCGCGGTG 1183

RESULT 9

US-09-214-808-1/c
 ; Sequence 1, Application US/09214808A
 ; Patent No. 6475793
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosenthal, Andre
 ; APPLICANT: Freiberg, Christoph
 ; APPLICANT: Perret, Xavier Philippe
 ; APPLICANT: Broughton, William John
 ; TITLE OF INVENTION: Genomic Sequence of Rhizobium SP. NGR 234 Symbiotic
 ; Patent No. 6475793
 ; TITLE OF INVENTION: Plasmid
 ; FILE REFERENCE: CARP0068
 ; CURRENT APPLICATION NUMBER: US/09/214,808A
 ; CURRENT FILING DATE: 1999-08-22
 ; PRIOR APPLICATION NUMBER: PCT/IB97/00950
 ; PRIOR FILING DATE: 1997-07-10
 ; NUMBER OF SEQ ID NOS: 1
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 536165
 ; TYPE: DNA
 ; ORGANISM: Rhizobium
 ; US-09-214-808-1

US-10-659-782A-32 (1-116) x US-09-214-808-1 (1-536165)

QY 3 SerProGlyThrVal-CysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeuAlaMe 22
 Db 82810 GCTCTGTGATCGGCTTGTCTG-----TTGCACTGGCGGCC 82775
 QY 22 tAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProProHisly 42
 Db 82774 GGTGTGATCAGCGGCTTCAGACATCTTCCGACTTGTGAACCGGTTCCGCCCGCA 82715
 QY 42 sAla-----ProHisValValProAlaLeuPr 51
 Db 82714 AGCCTTCATGCTTTCGCGCGGAAACAGATCGCTCGGCGCATCGGAGCGGCATTGCC 82655
 QY 51 oLeuSerAsnGlnLeuCysAspLeuGluGlnGlnArgHis-----Trp----- 65
 Db 82654 GCGGTAAACAGATCTGTTTCATCGGCGCGCATCGGAGAACTTCGTGTGCTGATCAG 82595
 QY 66 -----AlaSerValPheSerGlnSerThrLysAspSer-----GlySerAs 79
 Db 82594 CGGTCGAGCGGCCAGTTGCTTCGAGCGGCTCTTCGAGGATCCCTTCGTTGAAAACTGCG 82535
 QY 79 pleuThrValSer-GlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProS 99
 Db 82534 GCTGACCTGGTGCATCTCGACCGTGTGTCATCGCCAGCCCTCGAGATATAGTCCGCCGT 82475
 QY 99 erSerArgGluArgSerArgArgSerHisGlnProSer-----CysSerP 114
 Db 82474 CTCGGATCGTGTGATCGGCGCAACAGAAATCCAGCTCGGCTCTCGAACCATTTGCTCC 82415
 QY 114 roGluLeu 116
 Db 82414 CGCGTCTC 82407
 RESULT 10
 US-09-252-991A-13395/c
 ; Sequence 13395, Application US/09252991A


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; APPLICANT: Jono, Keith E.
; APPLICANT: Plowman, Gregory
; TITLE OF INVENTION: KINASE GENES AND USES
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FASTSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976,255
; FILING DATE: No. 6136581ember 21, 1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031,675
; FILING DATE: No. 6136581ember 22, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 229/182
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5267 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-976-255-2

Alignment Scores:
Pred. No.: 29.5 Length: 5267
Score: 81.50 Matches: 37
Percent Similarity: 29.2% Conservative: 11
Best Local Similarity: 22.56% Mismatches: 53
Query Match: 13.23% Indels: 63
DB: 3 Gaps: 6

US-10-659-782A-32 (1-116) x US-08-976-255-2 (1-5267)

QY 14 GlyMetLeuTrpLeuAspLeuAlaMetAlaGlySer-----SerPheLeu 28
DB 4355 GGGCTTTAGGCTTGTCTAGCCCTTGGGGCGCTGGAGCCAGTGGGGTGTCTGTAC 4414

QY 29 SerProGluHisGlnArgValGlnValArgProHisLysAlaProHisValPro 48
DB 4415 ACACATACACATCAAAAGGGCCAGTGCCTTGGCGACGGCGGCCGCCACCTCTGCC 4474

QY 49 AlaLeuPro---LeuSerAsnGlnLeuCysAspLeuGluGln----- 61
DB 4475 TGCCTGCTGGCTCGGAGGACCCGATGCCCATCCCGCAGCTCTCTCGGTGTGTCTAC 4534

QY 62 -----GlnArgHisTrpAlaSerValPheSerGln 71
DB 4535 AGGACATTAAACAGGACGAGGCATGGCCCCGACACACTGGCAGGTTGTGAGCCTCTT 4594

QY 72 SerThrLysAspSerGlySer-----AspLeuThrValSerGlyArgThrTrp--- 87
DB 4595 CCCACCCCTGTGCCCCACCTTGCCTGGTTCCTGGTGGCTCAGGGGACAGAGTGGCCC 4654

QY 87 ----- 87

Db 4655 TGGGCGCCCGTGTGGTCTGCTTTCCTGCTCCCTTATCTCAAGTCCGCTGTTTCCC 4714
QY 88 -----GlyLeuArgValLeuAenArgLeuPhePro 97
Db 4715 CTTCACTGACTAGTACCGTAAAGCCACCTTCCACAGGAGACAGGCTGCTCCCA 4774
QY 98 ProSerSerArg-----GluArgSerArgArgSerHisGlnPro 110
Db 4775 CCGTGGTCCCGCTGTGGCCAGCGTGGGAGCCCAAAAGATCAGGGGTGGAGGGCTTCCA 4834
QY 111 SerCysSerPro 114
Db 4835 GGCTGTACTCT 4846

RESULT 14
US-09-732-025-3
; Sequence 3, Application US/09732025
; Patent No. 6416990
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001011
; CURRENT APPLICATION NUMBER: US/09/732,025
; CURRENT FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 8285
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(8285)
; OTHER INFORMATION: n = A,T,C or G
US-09-732-025-3

Alignment Scores:
Pred. No.: 66.4 Length: 8285
Score: 81.00 Matches: 36
Percent Similarity: 37.21% Conservative: 12
Best Local Similarity: 27.91% Mismatches: 46
Query Match: 13.15% Indels: 36
DB: 4 Gaps: 4

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QY 1 MetProSerProGlyThrValCysSer-----LeuLeuLeuLeuGly 14
DB 6017 CTCCTCAAGCCAGGCACACC-TGCACAAACCCAGAGCCGCCCTCAGCTGCTCTAGGA 6075
QY 15 MetLeuTrpLeuAspLeuAlaMetAlaGlySerSerPheLeuSerProGluHisGlnArg 34
DB 6076 CACCTG----- 6081
QY 35 ValGlnValArgProProHisLysAlaProHisValValProAlaLeuProLeuSerAsn 54
DB 6082 -----TGCAGGTCTCCAGACCCAGGCCCCAGAGCAGCCAGCCACCTTCTGCTGT 6135
QY 55 GlnLeuCysAspLeu-----GluGlnGlnArgHisTrpAlaSerVal 68
DB 6136 ACGTGTGTGATCTTTGTGTCGCCGCCAGCGGAGCATGGCCGCCCTTCTGCTGT 6195
QY 69 PheSerGlnSerThrLysAspSerGlySerLeuThrValSerGlyArgThrTrpGly 88
DB 6196 GCTGCCAATAATGCGCAGCATTCGTTCTGACCCCTGGGGTTGACCCACTGACCCCGGG 6255
QY 89 LeuArgValLeuAenArgLeuPheProProSerArgGluArgSerArg----- 105
DB 6256 TTGACCACTGACCCACAGAGTCCCTGTCAGCAAGAACGTTCCAGGCAGAACATC 6315
QY 106 ArgSerHisGlnProSerCysSerPro 114

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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 10, 2005, 14:15:44 ; Search time 467 Seconds
(without alignments)
1427.244 Million cell updates/sec

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Perfect score: 616
Sequence: 1 MSPSTVCSLLLLGLMLDL.....PPSRRRRRRHQSPSPCL 116

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-Q=/cgn2_1/USPTO.spool/US10659782/runat_05022005_161919_4325/app_query.fasta_1.263
-DB=Published Applications NA -QWMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -LOCAL=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10659782 @CGN 1 1 480 @runat_05022005_161919_4325
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-XGAPOP=6 -FGAPEXT=7 -XGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:
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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:
6: /cgn2_6/ptodata/2/pubpna/PCTU5_PUBCOMB.seq:
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:
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10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:
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17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:
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19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:
20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:
21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

US-10-294-191A-11

Result No.	Score	Match	Length	DB ID	Description
1	220	35.7	447	15	US-10-294-191A-11
2	214	34.7	351	9	US-09-794-987-1
3	214	34.7	351	12	US-09-796-158-1
4	214	34.7	351	15	US-10-186-414-3
5	214	34.7	351	15	US-10-607-706-1
6	214	34.7	351	18	US-10-679-813-1
7	214	34.7	401	17	US-10-477-506-3
8	214	34.7	510	17	US-10-477-506-4
9	214	34.7	511	15	US-10-191-997-112
10	214	34.7	527	9	US-09-853-253-1
11	214	34.7	596	13	US-10-098-841-252
12	214	34.7	654	9	US-09-989-722-267
13	214	34.7	654	9	US-09-989-723-267
14	214	34.7	654	9	US-09-989-279-267
15	214	34.7	654	9	US-09-989-727-267
16	214	34.7	654	9	US-09-989-731-267
17	214	34.7	654	9	US-09-989-732-267
18	214	34.7	654	9	US-09-991-073-267
19	214	34.7	654	9	US-09-990-442-267
20	214	34.7	654	9	US-09-991-163-267
21	214	34.7	654	9	US-09-993-604-267
22	214	34.7	654	9	US-09-990-456-267
23	214	34.7	654	9	US-09-992-598-267
24	214	34.7	654	9	US-09-989-721-267
25	214	34.7	654	9	US-09-989-293A-267
26	214	34.7	654	9	US-09-989-735-267
27	214	34.7	654	9	US-09-990-444-267
28	214	34.7	654	9	US-09-991-181-267
29	214	34.7	654	9	US-09-989-730-267
30	214	34.7	654	9	US-09-990-436-267
31	214	34.7	654	9	US-09-993-687-267
32	214	34.7	654	10	US-09-989-734-267
33	214	34.7	654	10	US-09-997-653-267
34	214	34.7	654	10	US-09-989-724-267
35	214	34.7	654	10	US-09-989-728-267
36	214	34.7	654	10	US-09-990-441-267
37	214	34.7	654	10	US-09-993-667-267
38	214	34.7	654	10	US-09-997-428-267
39	214	34.7	654	10	US-09-997-666-267
40	214	34.7	654	10	US-09-990-438-267
41	214	34.7	654	10	US-09-990-562-267
42	214	34.7	654	10	US-09-990-711-267
43	214	34.7	654	10	US-09-989-726-267
44	214	34.7	654	10	US-09-998-156-267
45	214	34.7	654	10	US-09-990-437-267

ALIGNMENTS

RESULT 1
US-10-294-191A-11
; Sequence 11, Application US/10294191A
; Publication No. US20030211512A1
; GENERAL INFORMATION:
; APPLICANT: Rothschild, Max F.
; APPLICANT: Kim, Kwan Suk
; APPLICANT: Anderson, Lloyd L.
; TITLE OF INVENTION: Novel Ghrelin Alleles and Use of the Same for Genetically Typing
; FILE REFERENCE: P05408US1
; CURRENT APPLICATION NUMBER: US/10/294,191A
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: US 60/333,222
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; TYPE: DNA
; ORGANISM: Porcine

TELE

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; FILING DATE: 28-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION NUMBER: US/09/608,810
; PRIOR FILING DATE: 2000-06-30
; APPLICATION DATA:
;   APPLICATION NUMBER: 60/141,592
;   FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
;   NAME: Sawislak, Deborah A
;   REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-04
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 206-442-6672
;   TELEFAX: 206-442-6678
;   TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 351 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
;   NAME/KEY: sig_peptide
;   LOCATION: 1...351
; OTHER INFORMATION:
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-796-158-1

Alignment Scores:
Pred. No.:      1-39e-17      Length:      351
Score:          214.00        Matches:     51
Percent Similarity: 44.44%    Conservative: 1
Best Local Similarity: 43.59% Mismatches:      0
Query Match:     34.74%      Indels:         65
DB:              12          Gaps:           1

US-10-659-782A-32 (1-116) x US-09-796-158-1 (1-351)
Qy      1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuMetLeuTrpLeuAspLeu 20
Db      1 ATGCCCTCCCAGGACCGTCTGCAGCCCTCTCTCGGCATGCTCTGGCTGGACTTG 60
Qy      21 AlaMetAlaGlySerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
Db      61 GCCATGCGAGGTCCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAG----- 108
Qy      41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
Db      108 ----- 108
Qy      61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
Db      108 ----- 108
Qy      81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProSerSer 100
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Qy      101 Arg-GluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
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RESULT 4
US-10-186-414-3
; Sequence 3, Application US/10186414
; Publication No. US20030176640A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Deisher, Theresa A.
; TITLE OF INVENTION: SGIP PEPTIDES
; FILE REFERENCE: 99-51
; CURRENT APPLICATION NUMBER: US/10/186,414

; FILING DATE: 28-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION NUMBER: US/09/608,810
; PRIOR FILING DATE: 2000-06-30
; APPLICATION DATA:
;   APPLICATION NUMBER: 60/141,592
;   FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
;   NAME: Sawislak, Deborah A
;   REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-04
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 206-442-6672
;   TELEFAX: 206-442-6678
;   TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 351 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
;   NAME/KEY: sig_peptide
;   LOCATION: 1...351
; OTHER INFORMATION:
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-796-158-1

Alignment Scores:
Pred. No.:      1-39e-17      Length:      351
Score:          214.00        Matches:     51
Percent Similarity: 44.44%    Conservative: 1
Best Local Similarity: 43.59% Mismatches:      0
Query Match:     34.74%      Indels:         65
DB:              12          Gaps:           1

US-10-659-782A-32 (1-116) x US-09-796-158-1 (1-351)
Qy      1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuMetLeuTrpLeuAspLeu 20
Db      1 ATGCCCTCCCAGGACCGTCTGCAGCCCTCTCTCGGCATGCTCTGGCTGGACTTG 60
Qy      21 AlaMetAlaGlySerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
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Qy      41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
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Qy      61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
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Qy      81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProSerSer 100
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RESULT 5
US-10-607-706-1
; Sequence 1, Application US/10607706
; Publication No. US20030235887A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Deisher, Theresa A.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: TML Polynucleotides
; FILE REFERENCE: 97-04D3
; CURRENT APPLICATION NUMBER: US/10/607,706
; CURRENT FILING DATE: 2003-06-27
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/046,479
; PRIOR FILING DATE: 1998-03-28

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	FILING DATE:	28-Feb-2001
	CLASSIFICATION:	<Unknown>
	PRIOR APPLICATION NUMBER:	US/09608,810
	PRIOR FILING DATE:	2000-06-30
	APPLICATION DATA:	
	APPLICATION NUMBER:	09/046,479
	FILING DATE:	<Unknown>
	ATTORNEY/AGENT INFORMATION:	
	NAME:	Sawislak, Deborah A.
	REGISTRATION NUMBER:	37,438
	REFERENCE/DOCKET NUMBER:	97-04
	TELEPHONE:	206-442-6672
	TELEFAX:	206-442-6678
	TELEX:	<unknown>
	INFORMATION FOR SEQ ID NO: 1:	
	SEQUENCE CHARACTERISTICS:	
	LENGTH:	351 base pairs
	TYPE:	nucleic acid
	STRANDEDNESS:	single
	TOPOLOGY:	linear
	MOLECULE TYPE:	cDNA
	FEATURE:	
	NAME/KEY:	sig_peptide
	LOCATION:	1...351
	OTHER INFORMATION:	
	SEQUENCE DESCRIPTION:	SEQ ID NO: 1:
	US-09-796-158-1	
	Alignment Scores:	
	Pred. No.:	Length: 351 Score: 214.00 Matches: 51
	Percent Similarity:	44.44%
	Best Local Similarity:	Mismatches: 1
	Query Match:	Indels: 0
	DB:	Gaps: 65
	US-10-659-782A-32 (1-116) x US-09-796-158-1 (1-351)	
	Qy	1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuMetLeuTrpLeuAspLeu 20
	Dd	1 ATGCCCTCCCCAGGGACCGTCTGCAGCCCTCTGTCTCGCATGCTCTGGCTGGACTTG 60
	Qy	21 AlaMetAlaGlySerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
	Dd	61 GCCATGGCAAGTCCTGAGTTCTGTGAGCCCTGAACACCAGAGAGTCCAG----- 108
	Qy	41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
	Dd	108 ----- 108
	Qy	61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
	Dd	108 ----- 108
	Qy	81 ThrValserGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProSerSer 100
	Dd	108 ----- 108
	Qy	101 Arg-GluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
	Dd	109 CAGAGAAGAGTGCAGAAAGAACCCAGCACGCTGAGTCCAGCCCAGAGCTC 157
	RESULT 4	
	US-10-186-414-3	
	: Sequence 3, Application US/10186414	
	: Publication NO. US20030176640A1	
	: GENERAL INFORMATION:	
	: APPLICANT: Sheppard, Paul O.	
	: APPLICANT: Jaspers, Stephen R.	
	: APPLICANT: Deisher, Theresa A.	
	: APPLICANT: Bishop, Paul D.	
	: TITLE OF INVENTION: SGIP PEPTIDES	
	: FILE REFERENCE: 99-51	
	: CURRENT APPLICATION NUMBER: US/10/186,414	

Db 33 ATGCCCTCCCGAGGACCGCTCGCAGCCTCTGCTCGGCGATGCTCTGGCTGACTTG 92
Qy 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
Db 93 GCCATGGCAGGCTCCAGCTTCTGAGCCCTGAACACCCAGAGAGTCCAG----- 140
Qy 41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
Db 140 ----- 140
Qy 61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
Db 140 ----- 140
Qy 81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100
Db 140 ----- 140
Qy 101 Arg-GluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
Db 141 CAGAGAAAGGAGTCGAAGAAGCCACCCAGCTGCAGCCCGGAGCTC 189
RESULT 8
US-10-477-506-4
; Sequence 4, Application US/10477506
; Publication No. US20040157227A1
; GENERAL INFORMATION:
; APPLICANT: Chopin, Lisa K
; APPLICANT: Jeffery, Penelope L
; APPLICANT: Herington, Adrian C
; TITLE OF INVENTION: REPRODUCTIVE CANCER DIAGNOSIS AND THERAPY
; FILE REFERENCE: 225181
; CURRENT APPLICATION NUMBER: US/10/477,506
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: PR9567
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: PR4919
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: PCT/AU02/000582
; PRIOR FILING DATE: 2002-05-10
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 510
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-477-506-4
Alignment Scores:
Pred. No.: 2,198-17 Length: 510
Score: 214.00 Matches: 51
Percent Similarity: 44.44% Conservative: 1
Best Local Similarity: 43.59% Mismatches: 0
Query Match: 34.74% Indels: 65
DB: 17 Gaps: 1
US-10-659-782A-32 (1-116) x US-10-477-506-4 (1-510)
Qy 1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
Db 33 ATGCCCTCCCGAGGACCGCTCGCAGCCTCTGCTCGGCGATGCTCTGGCTGACTTG 92
Qy 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
Db 93 GCCATGGCAGGCTCCAGCTTCTGAGCCCTGAACACCCAGAGAGTCCAG----- 140
Qy 41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
Db 140 ----- 140
Qy 61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
Db 140 ----- 140

Qy 81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100
Db 140 ----- 140

Qy 101 Arg-GluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
Db 141 CAGAGAAAGGAGTCGAAGAAGCCACCCAGCTGCAGCCCGGAGCTC 189

RESULT 9

US-10-191-997-112
; Sequence 112, Application US/10191997
; Publication No. US20030207834A1

GENERAL INFORMATION:

; APPLICANT: Oligos Etc., Inc.
; APPLICANT: DALE, Roderic M. K.

; APPLICANT: ARROW, Amy

; APPLICANT: THOMPSON, Terry

; TITLE OF INVENTION: Oligonucleotide-Containing Pharmacological Compositions And Their

; FILE REFERENCE: 54800-5019

; CURRENT APPLICATION NUMBER: US/10/191,997

; CURRENT FILING DATE: 2002-07-10

; PRIOR APPLICATION NUMBER: US 60/303,820

; PRIOR FILING DATE: 2001-07-10

; NUMBER OF SEQ ID NOS: 132

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 112

; LENGTH: 511

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: NM_016362

US-10-191-997-112

Alignment Scores:

Pred. No.: 2,28-17 Length: 511
Score: 214.00 Matches: 51
Percent Similarity: 44.44% Conservative: 1
Best Local Similarity: 43.59% Mismatches: 0
Query Match: 34.74% Indels: 65
DB: 15 Gaps: 1

US-10-659-782A-32 (1-116) x US-10-191-997-112 (1-511)

Qy 1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
Db 34 ATGCCCTCCCGAGGACCGCTCGCAGCCTCTGCTCGGCGATGCTCTGGCTGACTTG 93

Qy 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
Db 94 GCCATGGCAGGCTCCAGCTTCTGAGCCCTGAACACCCAGAGAGTCCAG----- 141

Qy 41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
Db 141 ----- 141

Qy 61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
Db 141 ----- 141

Qy 81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100
Db 141 ----- 141

Qy 101 Arg-GluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
Db 142 CAGAGAAAGGAGTCGAAGAAGCCACCCAGCTGCAGCCCGGAGCTC 190

RESULT 10

US-09-853-253-1

; Sequence 1, Application US/09853253

; Patent No. US20020055156A1

```
; GENERAL INFORMATION:
; APPLICANT: JASPERS, STEPHEN
; APPLICANT: SHEPPARD, PAUL
; APPLICANT: DEISHER, THERESA
; APPLICANT: BISHOP, PAUL
; TITLE OF INVENTION: Zs1g33-like Peptides
; FILE REFERENCE: 00-30
; CURRENT APPLICATION NUMBER: US/09/853,253
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,300
; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 527
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (50)...(400)
US-09-853-253-1

Alignment Scores:
Pred. No.: 2,28e-17 Length: 527
Score: 214.00 Matches: 51
Percent Similarity: 44.44% Conservative: 1
Best Local Similarity: 43.59% Mismatches: 0
Query Match: 34.74% Indels: 65
DB: 9 Gaps: 1

US-10-659-782A-32 (1-116) x US-09-853-253-1 (1-527)
Qy 1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
Db 50 ATGCCCTCCCCAGGACCGCTGCAGCCTCCTGCTCGGCATGCTCTGGCTGGACTTG 109
Qy 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgPro 40
Db 110 GCCATGGCAGGCTCCAGCTTCTGAGCCCTGAACACACAGAGAGTCCAG----- 157
Qy 41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeu 60
Db 157 ----- 157
Qy 61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
Db 157 ----- 157
Qy 81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSer 100
Db 157 ----- 157
Qy 101 Arg-GluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
Db 158 CAGAGAAAGGAGTGAAGAACGCCACCAAGCTGCAGCCCGAGCTC 206

RESULT 11
US-10-098-841-252
; Sequence 252, Application US/10098841
; Publication No. US20020197679A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Xu, Chongjun
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yungqing
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhao, Qing A.
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
```

```
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20020197679A1el Nucleic Acids and
; FILE REFERENCE: 784CIP2
; CURRENT APPLICATION NUMBER: US/10/098,841
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 331
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 252
; LENGTH: 596
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (111)..(464)
US-10-098-841-252

Alignment Scores:
Pred. No.: 2,65e-17 Length: 596
Score: 214.00 Matches: 51
Percent Similarity: 44.44% Conservative: 1
Best Local Similarity: 43.59% Mismatches: 0
Query Match: 34.74% Indels: 65
DB: 13 Gaps: 1

US-10-659-782A-32 (1-116) x US-10-098-841-252 (1-596)
Qy 1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
Db 111 ATGCCCTCCCCAGGACCGCTGCAGCCTCCTGCTCGGCATGCTCTGGCTGGACTTG 170
Qy 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgPro 40
Db 171 GCCATGGCAGGCTCCAGCTTCTGAGCCCTGAACACACAGAGAGTCCAG----- 218
Qy 41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeu 60
Db 218 ----- 218
Qy 61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
Db 218 ----- 218
Qy 81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSer 100
Db 218 ----- 218
Qy 101 Arg-GluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
Db 219 CAGAGAAAGGAGTGAAGAACGCCACCAAGCTGCAGCCCGAGCTC 267

RESULT 12
US-09-989-722-267
; Sequence 267, Application US/09989722
; Patent No. US20020072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
```


APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC63
CURRENT APPLICATION NUMBER: US/09/989,722
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
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PRIOR FILING DATE: 1998-06-04
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PRIOR APPLICATION NUMBER: 60/088326
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PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
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PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
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PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
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PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
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PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472

; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090535
 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090540
 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090542
 ; PRIOR FILING DATE: 1998-06-24
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 ; PRIOR FILING DATE: 1998-06-25
 ; PRIOR APPLICATION NUMBER: 60/090678
 ; PRIOR FILING DATE: 1998-06-25
 ; PRIOR APPLICATION NUMBER: 60/090690
 ; PRIOR FILING DATE: 1998-06-25
 ; PRIOR APPLICATION NUMBER: 60/090694
 ; PRIOR FILING DATE: 1998-06-25
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 ; PRIOR FILING DATE: 1998-06-25
 ; PRIOR APPLICATION NUMBER: 60/090862
 ; PRIOR FILING DATE: 1998-06-26
 ; PRIOR APPLICATION NUMBER: 60/090863
 ; PRIOR FILING DATE: 1998-06-26
 ; PRIOR APPLICATION NUMBER: 60/091360
 ; PRIOR FILING DATE: 1998-07-01
 ; PRIOR APPLICATION NUMBER: 60/091478
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091544
 ; PRIOR FILING DATE: 1998-07-01
 ; PRIOR APPLICATION NUMBER: 60/091519
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091626
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091633
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091978
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

Alignment Scores:
 Pred. No.: 2,97e-17 Length: 654
 Score: 214.00 Matches: 51
 Percent Similarity: 44.44% Conservative: 1
 Best Local Similarity: 43.59% Mismatches: 0
 Query Match: 34.74% Indels: 65
 DB: 9 Gaps: 1

US-10-659-782A-32 (1-116) x US-09-989-722-267 (1-654)

QY 1 MetProSerProGlyThrValCysSerLeuLeuGlyWetLeuTrpLeuAspLeu 20
 DB 176 ATGCCCTCCCGAGGACCTGCGACCTCTGCTCGGATGCTCTGGCTGACTTG 235
 QY 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
 DB 236 GCATGGCAGGCTCCAGCTTCTGAGCCCTGACACCCAGAGATCCAG----- 283
 QY 41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
 DB 283 ----- 283
 QY 61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
 DB 283 ----- 283
 QY 81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProSerSer 100
 DB 283 ----- 283

QY 101 Arg-GluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
 DB 284 CAGAGAAAGGAGTGGAGAGAGCCACCCAGGCTGCGAGCCCGAGCTC 332
 RESULT 13
 US-09-989-723-267
 ; Sequence 267, Application US/09989723
 ; Patent No. US20020072092A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730PLC62
 ; CURRENT APPLICATION NUMBER: US/09/989,723
 ; CURRENT FILING DATE: 2001-11-19
 ; PRIOR APPLICATION NUMBER: 60/049787
 ; PRIOR FILING DATE: 1997-06-16
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/065186
 ; PRIOR FILING DATE: 1997-11-12
 ; PRIOR APPLICATION NUMBER: 60/065311
 ; PRIOR FILING DATE: 1997-11-13
 ; PRIOR APPLICATION NUMBER: 60/066770
 ; PRIOR FILING DATE: 1997-11-24
 ; PRIOR APPLICATION NUMBER: 60/075945
 ; PRIOR FILING DATE: 1998-02-25
 ; PRIOR APPLICATION NUMBER: 60/078910
 ; PRIOR FILING DATE: 1998-03-20
 ; PRIOR APPLICATION NUMBER: 60/083322
 ; PRIOR FILING DATE: 1998-04-28
 ; PRIOR APPLICATION NUMBER: 60/084600
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/087106
 ; PRIOR FILING DATE: 1998-05-28
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 ; PRIOR FILING DATE: 1998-07-09

Alignment Scores:
 Pred. No.: 2,97e-17 Length: 654
 Score: 214.00 Matches: 51
 Percent Similarity: 44.44% Conservative: 1
 Best Local Similarity: 43.59% Mismatches: 0
 Query Match: 34.74% Indels: 65
 DB: 9 Gaps: 1

US-10-659-782A-32 (1-116) x US-09-989-723-267 (1-654)

QY 1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20

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;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Alignment Scores:
Pred. No.: 2,97e-17 Length: 654
Score: 214.00 Matches: 51
Percent Similarity: 44.44% Conservative: 1
Best Local Similarity: 43.59% Mismatches: 0
Query Match: 34.74% Indels: 65
DB: 9 Gaps: 1

US-10-659-782A-32 (1-116) x US-09-989-279-267 (1-654)

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Db 236 GCCATGGCAGGCTCCAGCTTCTGAGCCCTGAACACGAGAGTCCAG----- 283
QY 41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
Db 283 ----- 283
QY 61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
Db 283 ----- 283
QY 81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100
Db 283 ----- 283
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RESULT 15
US-09-989-727-267
; Sequence 267, Application US/09989727
; Patent No. US20020072497A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavir, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC65

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 ; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

Alignment Scores:

Pred. No.:	2,97e-17	length:	654
Score:	214.00	Matches:	51
Percent Similarity:	44.44%	Conservative:	1
Best Local Similarity:	43.59%	Mismatches:	0
Query Match:	34.74%	Indels:	65
DB:	9	Gaps:	1

US-10-659-782A-32 (1-116) x US-09-989-727-267 (1-654)

QY	1	MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu	20
Db	176	ATGCCCTCCACGGACCGTCTGCTCTCGGCATGCTCTGGCTGGACTTG	235
QY	21	AlaMetAlaGlySerPheLeuSerProGluHisGlnArgValGlnValArgProPro	40
Db	236	GCCATGGCAGGCTCCAGCTTCTGAGCCCTGAACACAGAGAGTCCAG	283
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Search completed: February 10, 2005, 16:09:05
 Job time : 472 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 10, 2005, 13:45:44 ; Search time 2546 Seconds

(without alignments)
1660.255 Million cell updates/sec

Title: US-10-659-782A-32

Perfect score: 616

Sequence: 1 MPSPGTCVCSLLIGMLWLDL.....PPSSRRSRRRSHQSPSCSPEL 116

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=EST -Qfmt=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Database :

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2: gb_est2: *
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9: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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6	208.5	33.8	478	5	EX093784 EX093784
7	207	33.6	334	9	AY413164 Pan trogl
C 8	199.5	32.4	695	9	CE845760 tigr-gss-
9	190	30.8	542	4	BI907288 603063866

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	13	178	28.9	528	3	AK008860	AK008860 Mus muscu
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	19	170	27.6	334	9	AY413165	AY413165 Mus muscu
	20	169	27.4	404	5	BY096920	BY096920 BY096920
	21	165	26.8	758	9	AG071477	AG071477 Pan trogl
	22	164.5	26.7	343	5	BY112615	BY112615 BY112615
	23	164.5	26.7	370	5	BY083794	BY083794 BY083794
	24	160	26.0	330	5	BY149645	BY149645 BY149645
	25	157	25.5	294	2	BF543543	BF543543 UI-R-C3-c
	26	152	24.7	289	2	BB564523	BB564523 BB564523
	27	149.5	24.3	449	1	AI338429	AI338429 qq92a05.X
C	28	133.5	21.7	223	4	BI966558	BI966558 id55f03.X
	29	126	20.5	237	2	BB583439	BB583439 BB583439
C	30	109	17.7	419	1	AI057396	AI057396 ow75f03.X
C	31	106	17.2	558	7	CO055559	CO055559 TGESty06
C	32	104.5	17.0	635	9	CG311875	CG311875 OXCM40TV
C	33	104.5	17.0	667	9	CC636927	CC636927 OGBK53TV
C	34	104.5	17.0	813	9	CG338514	CG338514 OG2BF65TH
C	35	104	16.9	494	9	CG455078	CG455078 PUPX084TD
C	36	103.5	16.8	885	4	BI227046	BI227046 602952211
C	37	99	16.1	448	7	CN619603	CN619603 TGESty08
C	38	99	16.1	517	4	BG557206	BG557206 TGESty01
C	39	99	16.1	531	7	CK735827	CK735827 TGESty06
C	40	99	16.1	532	7	CK736563	CK736563 TGESty06
C	41	99	16.1	535	6	CB301576	CB301576 TGESty07
C	42	99	16.1	541	4	BG660654	BG660654 TGESty01
C	43	99	16.1	545	4	BM188954	BM188954 TGESty04
C	44	99	16.1	546	4	BM132122	BM132122 TGESty00
C	45	99	16.1	550	7	CK736357	CK736357 TGESty02

ALIGNMENTS

RESULT 1	BF929001	CM2-NT0185-071200-586-a07 NT0185 Homo sapiens cDNA, mRNA sequence.	431 bp	mRNA	linear	EST 19-JAN-2001
LOCUS	BF929001	CM2-NT0185-071200-586-a07 NT0185 Homo sapiens cDNA, mRNA sequence.	431 bp	mRNA	linear	EST 19-JAN-2001
DEFINITION	BF929001	CM2-NT0185-071200-586-a07 NT0185 Homo sapiens cDNA, mRNA sequence.	431 bp	mRNA	linear	EST 19-JAN-2001
ACCESSION	BF929001	CM2-NT0185-071200-586-a07 NT0185 Homo sapiens cDNA, mRNA sequence.	431 bp	mRNA	linear	EST 19-JAN-2001
VERSION	BF929001.1	GI:12327129	431 bp	mRNA	linear	EST 19-JAN-2001
KEYWORDS	EST.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	1 (bases 1 to 431)					
AUTHORS	Dias Neto, B., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.					
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags					
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.					
MEDLINE	20202663					
PUBLISHED	10717800					
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL					

(http://www.ludwig.org.br/scripts/gethtml2.pl?l1=CM2&t2=CM2-NT0185-071200-586-a07&t3=2000-12-07&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 8
 High quality sequence stop: 431.
 Location/Qualifiers

FEATURES

source

1..431
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="NT0185"
 /note="Organ: nervous tumor; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Alignment Scores:
 Pred. No.: 8 98e-44 Length: 431
 Score: 527.50 Matches: 101
 Percent Similarity: 99.02% Conservative: 0
 Best Local Similarity: 99.02% Mismatches: 0
 Query Match: 85.63% Indels: 1
 DB: 2 Gaps: 1

US-10-659-782A-32 (1-116) x BF929001 (1-431)

QY 16 LeuTrpLeuAspLeuAlaMetIaGlySerSerPheLeuSerProGluHisGlnArgVal 35
 Db 9 CTCCTGGCTGGACTTGGCCATGTCAGGCTCCAGCTTCTGAGCCCTCAACACCCAGAGATC 68
 QY 36 GlnValArgProHisIleValProHisValValProAlaLeuProLeuSerHengGln 55
 Db 69 CAGGTGAGACCTCCCAACAAAGCCACATGTGTTCAGCCCTGCCACTTAGCAACACAG 128
 QY 56 LeuCysAspLeuGluGlnArgHis---TrpAlaSerValPheSerGlnSerThrLys 74
 Db 129 CTCCTGACCTGGAGCAGCAGCGCCATCTCTGGGCTTCAGTCTTCTCCAGAGCAACAG 188
 QY 75 AspSerGlySerAspLeuThrValSerGlyArgThrTrpGlyLeuArgValLeuIleArg 94
 Db 189 GACTCTGGGCTGACCTCACTCTTCTGGAAGACATGGGGCTTAGAGTCTCTAAACAGA 248
 QY 95 LeuPheProSerSerArgGluArgSerArgSerHisGlnProSerCysSerPro 114
 Db 249 CTGTTTCCCTTCCAGCAGGAAAGGTCGAAGAAGCCACAGCAAGCTGCAGCCCC 308
 QY 115 GluLeu 116
 Db 309 GAGCTC 314

RESULT 2

AY413163

LOCUS

AY413163 Homo sapiens HCM4799 gene, VIRTUAL TRANSCRIPT, partial sequence,
 genomic survey sequence.

DEFINITION

AY413163

ACCESSION

AY413163

VERSION

GSS.

KEYWORDS

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

AUTHORS

TITLE

Inferring nonneutral evolution from human-chimp-mouse orthologous

gene trios
 Science 302 (5652), 1960-1963 (2003)
 14671302

JOURNAL

PUBMED

REFERENCE

AUTHORS

2 (bases 1 to 354)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,

Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,

Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,

Adams, M.D. and Cargill, M.

Direct Submission

Submitted (16-NOV-2003)

Celera Genomics, 45 West Gude Drive,

Rockville, MD 20850, USA

This sequence was made by sequencing genomic exons and ordering

them based on alignment.

Location/Qualifiers

source

1..354

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

<1..>354

/locus_tag="HCM4799"

gene

ORIGIN

Alignment Scores:

Pred. No.: 6 65e-12 Length: 354

Score: 214.00 Matches: 51

Percent Similarity: 44.44% Conservative: 1

Best Local Similarity: 43.59% Mismatches: 0

Query Match: 34.74% Indels: 65

DB: 9 Gaps: 1

US-10-659-782A-32 (1-116) x AY413163 (1-354)

QY 1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20

Db 1 ATGCCCTCCCGAGGACCGCTCTGCAGCCTCTCTCTCTCGCATCTCTGGCTGACTTG 60

QY 21 AlaMetIaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40

Db 61 GCCATGGCAGGCTCCAGCTTCTTGAGCCCTGAACACCCAGAGTCCAG----- 108

QY 41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60

Db 108 ----- 108

QY 61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80

Db 108 ----- 108

QY 81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProSerSer 100

Db 108 ----- 108

QY 101 Arg-GluArgSerArgSerHisGlnProSerCysSerProGluLeu 116

Db 109 CAGAGAAAGAGTTCGAAGAGCCACCCAGCAAGCTGCAGCCCGAGCTC 157

RESULT 3

BM854032

LOCUS

DEFINITION

K-EST0136326 S14K402 Homo sapiens cDNA clone S14K402-37-H03 5',

mRNA sequence.

ACCESSION

BM854032

VERSION

BM854032.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

AUTHORS

TITLE

21C Frontier Korean EST Project 2001

Inferring nonneutral evolution from human-chimp-mouse orthologous

JOURNAL
COMMENT

Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 37 row: H column: 03
High quality sequence stop: 526.
Location/Qualifiers

FEATURES
source

1. 526
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S14K402-37-H03"
/cell_line="K402"
/lab_host="Top10F"
/clone_lib="S14K402"
/note="Organ: Stomach; Vector: pTZ19RP1; Site 1: EcoRI;
Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tobacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dT-selected mRNA by
priming with dT-tailed vector. The dT-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

ORIGIN

Alignment Scores:
Pred. No.: 1.13e-11 Length: 526
Score: 214.00 Matches: 51
Percent Similarity: 44.44% Conservative: 1
Best Local Similarity: 43.59% Mismatches: 0
Query Match: 34.74% Indels: 65
DB: 4 Gaps: 1
US-10-659-782A-32 (1-116) x BM854032 (1-526)

QY 1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
|||
DB 50 ATGCCTCCCGAGGACCGCTGTCAGCCTCTCTCGGCATGCTCTGGCTGGACTTG 109
|||
QY 21 AlaMetAlaGlySerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
|||
DB 110 GCATGGAGCTCCAGCTTCCTGAGCCCTGAACACAGAGATCCAG----- 157
|||
QY 41 HisLysAlaProHisValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
----- 157
DB 61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
----- 157
DB 157 ----- 157
QY 81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100
----- 157
DB 157 ----- 157
QY 101 Arg-GluArgSerArgSerHisGlnProSerCysSerProGluLeu 116
::: |||
DB 158 CAGAGAAGAGAGTGGAGAGAGCCACCAGCAAGCTGCAGCCCGGAGCTC 206
|||

RESULT 4
BM982194/c

LOCUS
DEFINITION

BM982194 672 bp mRNA linear EST 21-FEB-2003
UI-CF-EN1-acr-k-05-0-UI-s1 UI-CF-EN1 Homo sapiens cDNA clone
UI-CF-EN1-acr-k-05-0-UI 3', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BM982194.1 GI:19605448
EST.
Homo sapiens (human)

REFERENCE
AUTHORS
TITLE

1 (bases 1 to 672)
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

JOURNAL
MEDLINE
PUBMED
COMMENT

Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
889548

FEATURES
source

Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source

1. 672
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-EN1-acr-k-05-0-UI"
/tissue_type="Primary Lung Cystic Fibrosis Epithelial
Cells"
/dev_stage="Adult"
/lab_host="UI-CF-EN1"
/clone_lib="UI-CF-EN1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-CF-EN1 is a normalized cDNA library containing the
following tissue(s): Primary Lung Cystic Fibrosis
Epithelial Cells. The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was ligated to an EcoR I adaptor, digested with Not
I, and cloned directionally into pT7T3-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is CTGCTCAGGT.
TAG_TISSUE=Human Lung Epithelial Cell lines untreated LPS
6hr to LPS 24h
TAG_LIB=UI-CF-EN1
TAG_SEQ=CTGCTCAGGT"

ORIGIN

Alignment Scores:
Pred. No.: 1.58e-11 Length: 672
Score: 214.00 Matches: 51
Percent Similarity: 44.44% Conservative: 1
Best Local Similarity: 43.59% Mismatches: 0
Query Match: 34.74% Indels: 65
DB: 5 Gaps: 1
US-10-659-782A-32 (1-116) x BM982194 (1-672)

sequence that is located between the Not I site and the (drr)18 tail. The sequence tag for this library is

ACACTTGCAC.
TAG TISSUE=chondrosarcoma
TAG LIB=UI-H-E11
TAG_SEQ=ACACTTGCAC"

ORIGIN

Alignment Scores:
Pred. No.: 1.6e-11 Length: 678
Score: 214.00 Matches: 51
Percent Similarity: 44.44% Conservative: 1
Best Local Similarity: 43.59% Mismatches: 0
Query Match: 34.74% Indels: 65
DB: 6 Gaps: 1

US-10-659-782A-32 (1-116) x CA449820 (1-678)

Qy 1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
Db 496 ATGCCCTCCCGAGGACCGCTCTGCAGCTCTCTCTCCGCGATGCTCTGGCTGAGCTTG 437
Qy 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
Db 436 GCCATGGCAGGCTCCAGCTTCTTGAGCCTCGAACACAGAGAGTCCAG----- 389
Qy 41 HisLysAlaProHisValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
Db 389 ----- 389
Qy 61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
Db 389 ----- 389
Qy 81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100
Db 389 ----- 389

Qy 101 Arg-GluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
Db 388 CAGAGAGAGAGTCCAGAGAGCCAGCCAGCCAGCTGCAGCCCGAGCTC 340

RESULT 6

LOCUS BX093784 478 bp mRNA linear EST 04-FEB-2003
DEFINITION BX093784 Soares total fetus ND2HF8_9w Homo sapiens cDNA clone
IMAGE:998E094758 ; IMAGE:1938800, mRNA sequence.

ACCESSION BX093784

VERSION BX093784.1 GI:27841729

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 478)

AUTHORS Ebert, J., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,
Radelof, U., Schneider, D. and Korn, B.

TITLE Human Unigeneset - RZPD3

JOURNAL Unpublished (2003)

COMMENT

Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany

RZPD; IMAGE:998E094758.

RZPDLIB; I.M.A.G.E. cDNA Clone Collection;

Human Unigeneset - RZPD3 (RZPDLIB No.972)

http://www.rzpd.de/CloneCards/cgi-

bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Heubenerweg 6, D-14059 Berlin, Germany

Tel: +49 30 32639 101

Fax: +49 30 32639 111

www.rzpd.de

This clone is available royalty-free from RZPD;

Qy 1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
Db 496 ATGCCCTCCCGAGGACCGCTCTGCAGCTCTCTCTCCGCGATGCTCTGGCTGAGCTTG 437
Qy 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
Db 436 GCCATGGCAGGCTCCAGCTTCTTGAGCCTCGAACACAGAGAGTCCAG----- 389
Qy 41 HisLysAlaProHisValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
Db 389 ----- 389
Qy 61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
Db 389 ----- 389
Qy 81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100
Db 389 ----- 389

Qy 101 Arg-GluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
Db 388 CAGAGAGAGAGTCCAGAGAGCCAGCCAGCTGCAGCCCGAGCTC 340

RESULT 5

CA449820/c

LOCUS

DEFINITION CA449820 678 bp mRNA linear EST 08-NOV-2002
UI-H-E11-ayy-c-12-0-UI-s1 NCI CGAP E11 Homo sapiens cDNA clone
UI-H-E11-ayy-c-12-0-UI 3', mRNA sequence.

ACCESSION CA449820

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 678)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. Jose Mercuende

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be obtained

from Dr. M. Bento Soares, bento-soares@uiowa.edu

Seq primer: M13 FORWARD

POLYA=Yes.

FEATURES

source

1..678

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="UI-H-E11-ayy-c-12-0-UI"

/tissue_type="Chondrosarcoma"

/dev_stage="Adult"

/lab_host="PH108 (Life Technologies)"

/clone_lib="NCI-CGAP_E11"

/note="Organ: Left Pelvis; Vector: pTT3-Pac (Pharmacia)

with a modified polylinker; Site 1: EcoR I; Site 2: Not I;

NCI-CGAP E11 is a normalized cDNA library containing the

following tissue(s): Chondrosarcoma. The library was

constructed according to Bonaldo, Lennon and Soares,

Genome Research, 6:791-806, 1996. First strand cDNA

synthesis was primed with an oligo-dT primer containing a

Not I site. Double stranded cDNA was ligated to an EcoR I

adaptor, digested with Not I, and cloned directionally

into pTT3-Pac vector. The oligonucleotide used to prime

the synthesis of first-strand cDNA contains a library tag

contact RZPD (clone@rzd.de) for further information. Seq primer:
M13r, Primer sequence: TTTCACAGCAAGAACGCTATGAC.

FEATURES

source
1..478
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE998E094758 ; IMAGE:1938800"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
/clone_lib="Soares total fetus Nb2HF8_9w"
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from pooled 8-9 week (total) fetus material with a Not I - oligo(dT) primer [5' TGTTACCAATCTCAAGTGGAGCGCGCTTAATTTTTTTTTTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Alignment Scores:
Pred. No.: 3.63e-11 Length: 478
Score: 208.50 Matches: 50
Percent Similarity: 43.59% Conservative: 1
Best Local Similarity: 42.74% Mismatches: 0
Query Match: 33.85% Indels: 66
DB: 5 Gaps: 1

US-10-659-782A-32 (1-116) x BX093784 (1-478)

QY 1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
|||||
DB 33 ATGCTCTCCCGAGGACCGTCTGAGCTCTCTCGCAAGCTCTGCTGGACTTG 92
QY 21 AlaMetAlaGlySerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
|||||
DB 93 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGATC----- 137
QY 41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
|||||
DB 137 ----- 137
QY 61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
|||||
DB 137 ----- 137
QY 81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100
|||||
DB 137 ----- 137
QY 101 Arg-GluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
::: |||||
DB 138 CAGAGAAAGGAGTTCGAAGAAGCCACCAGCAGCTGCAGCCCGAGCTC 186

RESULT 7

AY413164
LOCUS
DEFINITION
Pan troglodytes HCM4799 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.

ACCESSION
AY413164

VERSION
AY413164.1 GI:39769129

KEYWORDS
GSS.

SOURCE
Pan troglodytes (chimpanzee)

ORGANISM
Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Primates; Catarrhini; Hominidae; Pan.

1 (bases 1 to 334)

Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,

Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,

Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,

TITLE

Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios

JOURNAL

Science 302 (5652), 1960-1963 (2003)

PUBMED

14671302

AUTHORS

2 (bases 1 to 334)

Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,

Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,

Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,

Adams,M.D. and Cargill,M.

Direct Submission

JOURNAL

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,

Rockville, MD 20850, USA

This sequence was made by sequencing genomic exons and ordering

them based on alignment.

FEATURES

Location/Qualifiers

1..334

/organism="Pan troglodytes"

/mol_type="genomic DNA"

/db_xref="taxon:9598"

<1..->334

/locus_tag="HCM4799"

ORIGIN

US-10-659-782A-32 (1-116) x AY413164 (1-334)

Alignment Scores:
Pred. No.: 3.19e-11 Length: 334
Score: 207.00 Matches: 50
Percent Similarity: 43.59% Conservative: 1
Best Local Similarity: 42.74% Mismatches: 1
Query Match: 33.60% Indels: 65
DB: 9 Gaps: 1

QY 1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
|||||
DB 1 ATGCTCTCCCGAGGACCGTCTGAGCTCTCTCGCAAGCTCTGCTGGACTTG 60
QY 21 AlaMetAlaGlySerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
|||||
DB 61 GCCATGGCAGGCTCCAGCTTCCTGAGCCCTGAACACCAGAGATC----- 108
QY 41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
|||||
DB 108 ----- 108
QY 61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
|||||
DB 108 ----- 108
QY 81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100
|||||
DB 108 ----- 108
QY 101 Arg-GluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
::: |||||
DB 109 CAGAGAAAGGAGTTCGAAGAAGCCACCAGCAGCTGCAGCCCGAGCTC 157

RESULT 8

CE845760/c

LOCUS

DEFINITION

tigr-gss-dog-17000332741330 Dog Library Canis familiaris genomic,

genomic survey sequence.

ACCESSION

CE845760

VERSION

CE845760.1 GI:37208555

KEYWORDS

GSS.

SOURCE

Canis familiaris (dog)

ORGANISM

Canis familiaris

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

1 (bases 1 to 695)

Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,

Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and

Venter, J.C.
 The dog genome: survey sequencing and comparative analysis
 JOURNAL Science 301 (5641), 1898-1903 (2003)
 MEDLINE 22875432
 PUBMED 14512627
 COMMENT Contact: Kirkness EF
 The Institute for Genomic Research
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
 Rockville, MD 20850, USA
 Tel: 301-838-0200
 Fax: 301-838-0208
 Email: ekirknes@tigr.org
 Class: shotgun.
 Location/Qualifiers
 source
 1..695
 /organism="Canis familiaris"
 /mol_type="genomic DNA"
 /strain="Standard Poodle"
 /db_xref="taxon:9615"
 /clone_lib="Dog Library"
 /note="Site 1: BstXI; Libraries were prepared from
 peripheral blood"

ORIGIN

Alignment Scores:
 Pred. No.: 4,978-10 Length: 695
 Score: 199.50 Matches: 66
 Percent Similarity: 67.8% Conservative: 8
 Best Local Similarity: 60.5% Mismatches: 20
 Query Match: 32.3% Indels: 19
 DB: 9 Gaps: 6

US-10-659-782A-32 (1-116) x CE845760 (1-695)

QY 19 AspLeuAlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArg 38
 |||||
 Db 695 GACCTGGCCATCGCGGCTCCAGCTTCCTAGTCCCGAACACCAAGAACTACAGTAA- 637
 QY 39 Pro---ProHisGlyAlaProHis-----ValValProAlaLeuProLeu 52
 |||||
 Db 636 CCATCTCCCCACAAAGCCACG-TTTGGATTAGGTATCTGGCTCCAGCTTGCATGG 578
 QY 53 SerAsnGlnLeuCysAspLeuGlnGlnArgHisTrpAlaSerValPheSerGlnSer 72
 |||||
 Db 577 GGCAGCCAGCTGTGTGACCTTG--GCTCAAATTCTCTGGGCT------TTCTCCAAGAGC 526
 QY 73 ThrLys---AspSerGlySerAspLeu-----ThrValSerGlyArgThr 86
 |||||
 Db 525 ACTAAGGACACTCTGGGTCTGACTGTAGGCTCACACCTCCCTCTGCTTCTGGAAGTATA 466
 QY 87 TrpGlyLeuArgValLeuAsnArgLeuPheProProSerSerArgGluArgSerArgArg 106
 |||||
 Db 465 AGGGGGCTTAGGGCCCTA--AGATA-GTACCTTTTCCAGCAGAGAAAGGAGTCCAAGA 410
 QY 107 SerHisGlnProSerCysSerProGlu 115
 |||||
 Db 409 AGCCGCGCGCAAACTGCGAGCCCGAG 383

RESULT 9
 BI907288 542 bp mRNA- linear EST 16-OCT-2001
 LOCUS 603063866F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5212768 5',
 DEFINITION mRNA sequence.

ACCESSION BI907288
 VERSION BI907288.1 GI:16170099

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 542)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL COMMENT

Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILNL at:
<http://image.llnl.gov>
 Plate: L1AM11534 row: d column: 17
 High quality sequence stop: 535.

FEATURES

source

1..542
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5212768"
 /tissue_type="leukocyte"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_118"
 /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
 (destroyed); RNA source leukocytes from anonymous pool of
 non-activated adult donors. Library is oligo-dT primed
 and directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.7 kb, insert size range
 1.2-3.3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 027. Note:
 this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
 Pred. No.: 3,32e-09 Length: 542
 Score: 190.00 Matches: 50
 Percent Similarity: 43.5% Conservative: 1
 Best Local Similarity: 42.74% Mismatches: 1
 Query Match: 30.84% Indels: 66
 DB: 4 Gaps: 1

US-10-659-782A-32 (1-116) x BI907288 (1-542)

QY 1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
 |||||
 Db 40 ATGCTCTCCCGAGGACC-GTCTGCGAGCTCTCTCTCGGATGCTCTGGCTGACTTG 98
 QY 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
 |||||
 Db 99 GCCATGGCAGGCTCCAGCTTCTTGAGCTTGAACACAGAGAGTCCAG----- 146
 QY 41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
 |||||
 Db 146 ----- 146
 QY 61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
 |||||
 Db 146 ----- 146
 QY 81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100
 |||||
 Db 146 ----- 146
 QY 101 Arg-GluArgSerArgSerHisGlnProSerCysSerProGluLeu 116
 |||||
 Db 147 CAGAGAAAGGAGTCCAGAGAACCCAGCAGAGCTGCGAGCTGCGAGCTC 195

RESULT 10

AA530994/c

LOCUS

DEFINITION

mRNA sequence.

ACCESSION AA530994

VERSION AA530994.1 GI:2273700

AA530994 600 bp mRNA linear EST 20-AUG-1997
 nj07a01.s1 NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:985608 3',
 DEFINITION mRNA sequence.

	QY	104 SerArgSerHisGlnProSerCysSerProGluLeu 116 376 AGTCGAAGAAGCCACCAAGCTGCAGCCCGAGTTC 338
Db		
RESULT 11		
BY708559		
LOCUS		
DEFINITION		
MUSCULUS		
EST.		
BY708559.1	GI:27119750	
ACCESION		
VERSION		
KEYWORDS		
SOURCE		
ORGANISM		
REFERENCE		
AUTHORS		
Okaaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Oeato,N., Saito,R., Suzuki,H., Yamashita,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reid,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultanara,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tonita,M., Verardo,R., Wagner,B., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002) 22354683 12466851 Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/ Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Horii,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001) Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)		
Db		
RESULT 11		
BY708559		
LOCUS		
DEFINITION		
MUSCULUS		
EST.		
BY708559.1	GI:27119750	
ACCESION		
VERSION		
KEYWORDS		
SOURCE		
ORGANISM		
REFERENCE		
AUTHORS		
Okaaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Oeato,N., Saito,R., Suzuki,H., Yamashita,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reid,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultanara,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tonita,M., Verardo,R., Wagner,B., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002) 22354683 12466851 Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/ Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Horii,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001) Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)		
Db		
RESULT 11		
BY708559		
LOCUS		
DEFINITION		
MUSCULUS		
EST.		
BY708559.1	GI:27119750	
ACCESION		
VERSION		
KEYWORDS		
SOURCE		
ORGANISM		
REFERENCE		
AUTHORS		
Okaaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Oeato,N., Saito,R., Suzuki,H., Yamashita,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reid,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultanara,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tonita,M., Verardo,R., Wagner,B., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002) 22354683 12466851 Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/ Adachi,J., Aizawa,K., Akimura,T., Arakawa,T.,		

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES

Location/Qualifiers

1..523
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="2210006E23"
 /sex="male"
 /tissue type="stomach"
 /dev stage="adult"
 /lab_host="SOLR"
 /clone_lib="RIKEN full-length enriched, adult male stomach"
 /note="Site 1: XhoI; Site 2: SstI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGAGAGAGCGCGCAACTCGAGTTTATTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGATCTCGAGTTTATTTTNN 3']. cDNA was cleaved with XhoI and SstI."

ORIGIN

Alignment Scores:
 Pred. No.: 5,3e-08 Length: 523
 Score: 178.00 Matches: 54
 Percent Similarity: 45.71% Conservative: 10
 Best Local Similarity: 38.57% Mismatches: 39
 Query Match: 28.90% Indels: 37
 DB: 6 Gaps: 5

US-10-659-782A-32 (1-116) x BY708559 (1-523)

QY 1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20
 DB 40 ATGCTGCTTCAGGCACCATCTGCAGTTGCTACTCAGCATGCTCTGGATGGACATG 99
 QY 21 AlaMetAlaGlySerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
 DB 100 GCATGGCAGGCTCCAGCTTCTGAGCCAGAGCACCAGAACCCAGCAGAGAAGGAA 159
 QY 41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
 DB 160 TCCAGAAGGCCA-----CCAGCTAAACTGCAGCCAGCAGCTCTGGAA 201
 QY 61 GlnGlnArgHis----- 64
 DB 202 GCGTGGCTCCACCAGAGCAGACAGCAAGCAGAGACACAGAGGAGCTGGAGATC 261
 QY 65 ---TrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeuThrValSer 83
 DB 262 AGGTTCAATGCTCCCTTCAGTGTGGCATCAGCTCTCAGAGCTCAGTATCAGCAGCAT 321
 QY 84 GlyArgThr-TrpGlyLeuArgValLeuAsnArgLeuPheProProSerSerArgGluAr 103
 DB 322 GGCCTGGCCCTGGCGA-----AGTTCTTTCAGGATATCTCTCTGGGAAGAG 366
 QY 103 gSerArgArg-----SerHisGln-----ProSerCysSerPro 114

Db 367 GTCAAGAGGCGCGCAGCTGACAAGTAACCAAGGAGCGCTGACCCCGTCTTCTCT 424

RESULT 12
 AK008658
 LOCUS
 DEFINITION

AK008658 527 bp mRNA linear HTC 03-APR-2004
 Mus musculus adult male stomach cDNA, RIKEN full-length enriched library, clone:2210006E23 product:GHRELIN PRECURSOR, full insert sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

AK008658.1 GI:12842985
 HTC; CAP trapper.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1
 Carninci,P. and Hayashizaki,Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 99279253
 PUBMED 10349636

REFERENCE
 AUTHORS

Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
 20499374
 PUBMED 11042159

REFERENCE
 AUTHORS

Shibata,K., Itoh,M., Aizawa,K., Nagao,K., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsuai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishino,T., Harada,A., Yanamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multiplexed capillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 20530913
 PUBMED 11076861

REFERENCE
 AUTHORS

The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409, 685-690 (2001)

REFERENCE
 AUTHORS

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)

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Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukuishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,C., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Saito,H., Sato,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
 Direct Submission

REFERENCE
 AUTHORS

Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.jp)

Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

TITLE Direct Submission
JOURNAL Submitted (10-JUN-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gscc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT Please visit our web site (http://genome.gsc.riken.jp/) for further details.

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5'-GAGAGAGAGATTCGAGTTAAATTAATCCCGCCCCCCC 3'], cDNA was prepared by using thermostable thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'-GAGAGAGATTCGAGTTAAATTAATCCCGCCCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI. Host: SOLR.

FEATURES

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polyA_signal
/note="putative"
528
polyA_site
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ORIGIN

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Percent Similarity: 45.71% Conservative: 10
Best Local Similarity: 38.57% Mismatches: 39
Query Match: 28.90% Indels: 37
DB: 3 Gaps: 5

US-10-659-782a-32 (1-116) x AK008860 (1-528)

QY 1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTripleuAspLeu 20
Db 44 ATGCTGCTTCAGGCACCATCTGCAGTTGCTGCTACTCAGCATGCTCTGGATGACATG 103
QY 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
Db 104 GCATGGCAGGCTTCAGCTTCTGAGCCAGAGCCACCAAGAAAGGAGAA 163
QY 41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
Db 164 TCCAGAGAGCCA-----CCAGCTAAACTCCAGCCAGCAGCTCTGGAA 205

QY 61 GlnGlnArgHis----- 64
Db 206 GGCTGGCTCCACCCAGAGCAGAGGACAGAGCAAGAGAGAGAGAGAGAGAGCTGGAGATC 265
QY 65 ---TpaLaserValPheSerGlnSerThrLysAspSerGlySerAspLeuThrValSer 83
Db 266 AGTTTCATGCTCCCTTCGATGTTGGCATCAAGCTGTCAGGAGCTCAGTATCAGCAGCAT 325
QY 84 GlyArgThr-TrpGlyLeuArgValLeuAsnArgLeuPheProProSerSerArgGluArg 103
Db 336 GGCCGGGCGCTGGGA-----AGTTTCTTTCAGGATATCTCTGGGAGAG 370
QY 103 gSerArgArg-----SerHisGln-----ProSerCysSerPro 114
Db 371 GTCAAGAGAGGCGCCAGCTGACAAAGTAACCCAGGAGCGCCCTGACCCCGTCTTCTCT 428

RESULT 14

CK373838

LOCUS

DEFINITION

CK373838

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

Source

polyA_signal

polyA_site

ORIGIN

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

US-10-659-782a-32 (1-116) x AK008860 (1-528)

QY 1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTripleuAspLeu 20

Db 44 ATGCTGCTTCAGGCACCATCTGCAGTTGCTGCTACTCAGCATGCTCTGGATGACATG 103

QY 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40

Db 104 GCATGGCAGGCTTCAGCTTCTGAGCCAGAGCCACCAAGAAAGGAGAA 163

QY 41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60

Db 164 TCCAGAGAGCCA-----CCAGCTAAACTCCAGCCAGCAGCTCTGGAA 205

FEATURES

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polyA_signal

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ORIGIN

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Percent Similarity:

Best Local Similarity:

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DB:

US-10-659-782a-32 (1-116) x AK008860 (1-528)

QY 1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTripleuAspLeu 20

Db 44 ATGCTGCTTCAGGCACCATCTGCAGTTGCTGCTACTCAGCATGCTCTGGATGACATG 103

QY 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40

Db 104 GCATGGCAGGCTTCAGCTTCTGAGCCAGAGCCACCAAGAAAGGAGAA 163

QY 41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60

Db 164 TCCAGAGAGCCA-----CCAGCTAAACTCCAGCCAGCAGCTCTGGAA 205

FEATURES

Source

polyA_signal

polyA_site

ORIGIN

Alignment Scores:

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DB:

US-10-659-782a-32 (1-116) x AK008860 (1-528)

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